

GenCore version 5.1.8  
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OMP protein - protein search, using sw model

Run on: May 19, 2006, 17:34:57 ; Search time 158.667 Seconds  
(without alignments)  
391.900 Million cell updates/sec

Title: US-09-889-936A-6  
Perfect score: 737  
Sequence: 1 MRVLILLWLTAFPGILSDV.....WDYGTTYGYFDVWGQTTVT 136

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A Geneseq 8:\*
- 1: geneseqp1980s:\*
  - 2: geneseqp1990s:\*
  - 3: geneseqp2000s:\*
  - 4: geneseqp2001s:\*
  - 5: geneseqp2002s:\*
  - 6: geneseqp2003as:\*
  - 7: geneseqp2003bs:\*
  - 8: geneseqp2004s:\*
  - 9: geneseqp2005s:\*
  - 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	737	100.0	136	AAB15672	Aab15672 Murine 5B
2	627.5	85.1	468	ADY91369	Ady91369 Anti-KID3
3	622.5	84.5	136	ADZ81889	Adz81889 Anti-lami
4	593.5	80.5	130	10 AEE98109	Aee98109 Murine PE
5	588.5	79.9	136	2 AAW01144	Aaw01144 MAb 1.4 h
6	588.5	79.9	136	2 AAW44169	Aaw44169 Monoclona
7	588	79.8	137	2 AAR28671	Aar28671 pPM-hl pr
8	586.5	79.6	134	6 ABB82796	Abb82796 Antibody
9	569.5	77.3	255	8 ADS14282	Adsl4282 Murine pr
10	569.5	77.3	519	8 ADS14288	Adsl4288 Murine pr
11	556.5	75.5	120	8 ADO44274	Ado44274 Consensus
12	556.5	75.5	120	8 ADO44271	Ado44271 Sequence
13	554	75.2	127	7 ADJ76886	Adj76886 Anti-IGF-
14	554	75.2	127	9 ADZ67056	Adz67056 Murine im
15	554	75.2	127	9 AEE61302	Aee61302 Murine mo
16	552.5	75.0	119	8 ADO44272	Ado44272 Primer in
17	544.5	73.9	120	8 ADO44280	Ado44280 Humanised
18	544.5	73.9	122	8 ADL26964	Adl26964 Mouse ant
19	544	73.8	121	6 ABP59986	Abp59986 Antibody
20	544	73.8	121	7 ADF69650	Adf69650 Humanised
21	544	73.8	121	9 AEB03869	Aeb03869 B-CuL pha
22	544	73.8	121	9 AEE17798	Aee17798 Anti-huma
23	541	73.4	119	2 AAW01584	Aaw01584 Lead bind

24	539.5	73.2	730	9 AEC08410	Aec08410 SCFv-B2-F
25	539.5	73.2	730	9 AEC08411	Aec08411 SCFv-B2-F
26	539.5	73.2	761	9 AEC08409	Aec08409 SCFv-A12A
27	539.5	73.2	762	9 AEC08408	Aec08408 SCFv-B2-F
28	537.5	72.9	154	9 ABE17974	Aee17974 Murine SC
29	535.5	72.7	140	2 AAW21937	Aaw21937 Variable
30	535.5	72.7	140	2 AAY05267	Aay05267 Antibody
31	535.5	72.7	140	5 ABG98318	Abg98318 Murine wi
32	533.5	72.4	539	8 ADR42630	Adr42630 Mouse ant
33	533	72.3	522	9 AEC20775	Aec20775 M-CSF spe
34	532.5	72.3	115	7 ADJ80371	Adj80371 Murine an
35	531.5	72.1	118	9 ADZ81874	Adz81874 Anti-lami
36	529.5	71.8	122	9 ADW14662	Adw14662 Anti-comp
37	529	71.8	126	2 AAR24722	Aar24722 Sequence
38	528.5	71.7	118	9 AEC20767	Aec20767 M-CSF spe
39	528.5	71.7	447	9 AEC20763	Aec20763 M-CSF spe
40	527.5	71.6	118	7 ADJ76904	Adj76904 Anti-IGF-
41	527.5	71.6	118	9 ADZ67074	Adz67074 Mouse ant
42	527.5	71.6	118	9 ABE61320	Aee61320 Murine mo
43	526.5	71.4	114	9 ADZ81898	Adz81898 Mouse ant
44	526	71.4	117	8 ADU39968	Adu39968 Antibody
45	525.5	71.3	117	2 AAR07318	Aar07318 VH domain

ALIGNMENTS

RESULT 1  
AAB15672  
ID AAB15672 standard; protein; 136 AA.  
XX  
AC AAB15672;  
XX  
DT 08-JAN-2001 (first entry)  
XX  
DE Murine 5B3 antibody heavy chain variable region.  
XX  
KW Mouse; 5B3 antibody; IgG1; piezoelectric immunoassay;  
KW small molecule explosive detection; 2,4,6-trinitrotoluene; TNT.  
XX  
OS Mus sp.  
XX  
PN WO200043774-A2.  
XX  
PD 27-JUL-2000.  
XX  
PF 25-JAN-2000; 2000WO-IL000048.  
XX  
PR 25-JAN-1999; 99IL-00128212.  
XX  
(YISS ) YISSUM RES & DEV CO.  
(YEDA ) YEDA RES & DEV CO LTD.  
PI Willner I, Eshhar Z;  
XX  
DR WPI; 2000-524259/47.  
DR N-PSDB; AAA74604.  
XX  
PT Apparatus for detecting small molecules, especially explosives comprises a piezoelectric crystal.  
XX  
PS Disclosure; Fig 3A; 90pp; English.  
XX  
CC The present sequence is the heavy chain variable region of 5B3 antibody.  
CC The cDNA encoding this sequence was obtained from total RNA extracted from a 5B3 hybridoma by RT-PCR. 5B3 is an IgG1 antibody derived from a TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked by very low amounts of TNT and it can therefore be used in a method for detecting small assayed explosive molecules. Molecules are detected using a piezoelectric sensor. Piezoelectric immunoassaying in liquid phase allows stationary and flow analysis of an aqueous sample. The method is sufficiently sensitive for detection of low molecular weight molecules

XX







CC polypeptide encoded by the PERP gene. The disease is cancer. The antibody  
CC is useful in diagnosing a disease by detecting or measuring the amount of  
CC a polypeptide encoded by the PERP gene in a cell, for treating cancer,  
CC for manufacturing a diagnostic, for detecting cancer and for  
CC manufacturing a therapeutic agent for cancer. This sequence represents a  
CC murine PERP related protein of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 130 AA;

Query Match 80.5%; Score 593.5; DB 10; Length 130;  
Best Local Similarity 81.6%; Pred. No. 1.3e-47;  
Matches 111; Conservative 10; Mismatches 6; Indels 9; Gaps 1;

QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYISITSGYAWNWIROQPP 60  
Db |||||  
QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCTVTGFSITTEYAWNWIROQPP 60  
Db |||||  
QY 61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQNSVTSEDTATYYCARWDYG 120  
Db |||||  
QY 61 GNRLEWMGYIGYTGRTNYSPLKSRISITRDTSKNQFFLQNSVTTEDTATYYCTRMDY- 119  
QY 121 TTYGYFDVWGQGTTVT 136  
Db |||||

RESULT 5  
AAW01144  
ID AAW01144 standard; protein; 136 AA.

XX AAW01144;

DT 10-FEB-1997 (first entry)

DE Mab 1.4 heavy chain, directed against type II phospholipase A2.

XX Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis;  
KW cerebral infarction; acute kidney failure; colitis; chronic rheumatism;  
KW adult respiratory distress syndrome; cardiac shock; treatment;  
KW preclinical testing; disease; hybridoma.

XX Mus musculus.

OS Key Location/Qualifiers  
FH Binding-site 49..54  
FT /label= CDR 1  
FT Binding-site 69..84  
FT /label= CDR 2  
FT Binding-site 117..125  
FT /label= CDR 3

XX WO9620959-A1.

XX 11-JUL-1996.

PF 27-DEC-1995; 95WO-JP002714.

PR 29-DEC-1994; 94JP-00340006.

XX (YAMA ) YAMANOUCHI PHARM CO LTD.

PI Kawauchi Y, Takasaki J, Yasunaga T, Masuho Y;

XX WPI; 1996-333946/33.

DR N-PSDB; AAT40804.

XX Monoclonal antibody inhibiting type II phospholipase A2 activity - for

PT treatment of myocardial and cerebral infarction.

XX Claim 6; Fig 11; 69pp; Japanese.

XX Monoclonal antibodies which inhibit type II phospholipase A2 are useful  
CC in the treatment of myocardial infarction, cerebral infarction, acute  
CC kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult  
CC respiratory distress syndrome and colitis. The antibodies were generated  
CC by immunising Balb/C mice with recombinant human type II phospholipase  
CC A2. Spleen cells from the mice were fused with mouse myeloma P3U1  
CC (P3x63Ag8.U1) and the hybridomas obtained were screened for phospholipase  
CC A2 inhibitory activity. Active clones were isolated including 12H5, 1.4  
CC and 10.1. These were cultured and the antibody isolated from the culture  
CC supernatant by precipitation with ammonium sulphate and purification on a  
CC column of protein A-Sepharose CL4B. Because the antibody acts on the  
CC primate and mouse forms of enzyme as well as human it is particularly  
CC suitable for preclinical testing

XX Sequence 136 AA;

Query Match 79.9%; Score 588.5; DB 2; Length 136;  
Best Local Similarity 81.4%; Pred. No. 4.1e-47;  
Matches 114; Conservative 4; Mismatches 11; Indels 11; Gaps 2;

QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYISITSGYAWNWIROQPP 60  
Db |||||  
QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCMVTGYISITSDYAWNWIROQPP 60  
Db |||||  
QY 61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQNSVTSEDTATYYCAR---- 116  
Db |||||  
QY 61 GNRLEWMGYIRYSGYTSYNPSLKSRIFFITRDTSQNQFFLHLTSVTTEDTATYYCTRDLD 120  
QY 117 WDYGTTYGYFDVWGQGTTVT 136  
Db |||||

RESULT 6  
AAW44169  
ID AAW44169 standard; protein; 136 AA.

XX AAW44169;

DT 16-JUN-1998 (first entry)

XX Monoclonal antibody 1.4 heavy chain against type II phospholipase A2.

XX Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;  
KW amelioration; kidney disorder; nephrotoxicity; anticancer.

XX Unidentified.

XX WO9749427-A1.

XX 31-DEC-1997.

XX 27-JUN-1997; 97WO-JP002241.

PR 27-JUN-1996; 96JP-00167286.

PR 19-SEP-1996; 96JP-00247635.

XX (YAMA ) YAMANOUCHI PHARM CO LTD.

XX Kawauchi Y, Takasaki J, Hayashi K, Masuho Y;

DR WPI; 1998-076914/07.

DR N-PSDB; AAV12261.

XX Amelioration of kidney disorders caused by cisplatin administration - by  
PT treatment with an antibody inhibiting type II phospholipase A2 activity.

XX Disclosure; Page 38; 74pp; Japanese.

XX The present sequence represents the monoclonal antibody 1.4 heavy chain  
CC against type II phospholipase A2, from the present invention. The present  
CC invention describes a novel method for the amelioration of kidney



CC disorders (such as acute renal failure) associated with the  
CC administration of cisplatin for the treatment of cancer. The method  
CC comprises treatment with a monoclonal antibody which inhibits the  
CC activity of type II phospholipase A2 (particularly of type II  
CC phospholipase A2 of human origin), or with a protein or peptide  
CC possessing the same inhibitory activity and containing a part of the  
CC antibody sequence. Preferably the antibody also inhibits the activity of  
CC type II phospholipase A2 bound to a cell membrane. Three specific  
CC monoclonal antibodies having these properties which can be used are 12H5,  
CC 10.1 and 1.4, derived from hybridomas FERM BP-5300, FERM BP-5298 and FERM  
CC BP-5297 respectively. The method can be used for suppressing the  
CC nephrotoxicity which is a characteristic feature of cisplatin  
CC administration, and therefore allowing more efficient use of this drug as  
CC an anticancer agent, e.g. by allowing an increased dosage to be used  
XX  
SQ Sequence 136 AA;

Query Match 79.9%; Score 588.5; DB 2; Length 136;  
Best Local Similarity 81.4%; Pred. No. 4.1e-47;  
Matches 114; Conservative 4; Mismatches 11; Indels 11; Gaps 2;  
QY 1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLTCSVTGYISITSGYAWNWIROFP 60  
Db 1 MRVLILLWLFTAFPGFLSDVQLQESGPGLVKPSQSLTCTMTGYISITSDYAWNWIROFP 60  
QY 61 GNKLEWMGYISYSGFTSYNPSLSRISFTRDTSKNQFFLQNSVTSEDATYYCAR--- 116  
Db 61 GNKLERMGYIRYSGYTSYNPSLSKSRIFITRDTSQNFHLTTSVTTEDATYYCTRDLLA 120  
QY 117 WDYGTTYGYFDVWGQGTTVT 136  
Db 121 W-----YFDVWGAGTTVT 133

RESULT 7  
AAR28671  
ID AAR28671 standard; protein; 137 AA.  
XX  
AC AAR28671;  
XX  
DT 25-MAR-2003 (revised)  
DT 30-MAR-1993 (first entry)  
XX  
DE ppm-h1 protein product.  
XX  
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;  
KW heavy chain; variable region; mouse; monoclonal; hybridoma; PM1; plasmid;  
KW ppm-k3; ppm-h1.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .18  
FT /note= "Signal peptide"  
FT Protein 19. .137  
FT /note= "Mature peptide"  
XX  
PN WO9219759-A1.  
XX  
PD 12-NOV-1992.  
XX  
PF 24-APR-1992; 92WO-JP000544.  
XX  
PR 25-APR-1991; 91JP-00095476.  
PR 19-FEB-1992; 92JP-00032084.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tauchiya M, Sato K, Bendig MM, Jones ST, Saldanha JW;  
XX  
DR WPI; 1992-398882/48.  
DR N-PSDB; AAQ30756.

XX Reconstituted human antibody to human interleukin-6 receptor - has low  
PT antigenicity and contains mouse V-region complementarily determining  
PT regions.  
XX Disclosure; Page 122-123; 207pp; Japanese.  
XX  
CC The sequences given in AAR28670-71 were encoded by plasmids which were  
CC used in example to illustrate the production of a human antibody which  
CC recognises human interleukin-6 receptor (IL-6R). The antibody comprises  
CC light (L) chain and heavy (H) chain variable regions which were derived  
CC from a mouse monoclonal antibody produced from the hybridoma PM1 which  
CC contained the plasmids ppm-k3 and ppm-h1. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX  
SQ Sequence 137 AA;

Query Match 79.8%; Score 588; DB 2; Length 137;  
Best Local Similarity 83.8%; Pred. No. 4.6e-47;  
Matches 114; Conservative 8; Mismatches 12; Indels 2; Gaps 1;  
QY 1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLTCSVTGYISITSGYAWNWIROFP 60  
Db 1 MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLTCTVTGYISITSDHAWSWIROFP 60  
QY 61 GNKLEWMGYISYSGFTSYNPSLSRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYG 120  
Db 61 GNKLEWMGYISYSGITTYNPSLSKSRISITRDTSKNQFFLQNSVTGDTSTYYCARSLAR 120  
QY 121 TTYGYFDVWGQGTTVT 136  
Db 121 TT--AMDYWGQGTSTVT 134

RESULT 8  
ABB82796  
ID ABB82796 standard; protein; 134 AA.  
XX  
AC ABB82796;  
XX  
DT 18-MAR-2003 (first entry)  
XX  
DE Antibody 806 variable heavy chain (VH) region.  
XX  
KW Epidermal growth factor receptor; EGFR; tumourigenic; cytostatic;  
KW monoclonal antibody; mAb 806; antibody therapy; tumour.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .18  
FT /note= "signal peptide"  
FT Protein 19. .134  
FT /note= "mAb 806 VH region"  
XX  
PN WO200292771-A2.  
XX  
PD 21-NOV-2002.  
XX  
PF 13-MAY-2002; 2002WO-US015185.  
XX  
PR 11-MAY-2001; 2001US-0290410P.  
PR 28-SEP-2001; 2001US-0326019P.  
PR 21-DEC-2001; 2001US-0342258P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX  
PI Old LJ, Johns TG, Panoueis C, Scott AM, Renner C, Ritter G;  
PI Jungbluth A, Stockert E, Collins P, Cavenee WK, Huang H, Burgess AW;  
PI Nice EC;  
XX  
DR WPI; 2003-129282/12.  
DR N-PSDB; ABZ23940.

Novel specific binding members, particularly antibodies recognizing epidermal growth factor receptor epitope found only in tumorigenic cells, useful for diagnosing, preventing and treating cancer in mammals.

Claim 6; Fig 14B; 123pp; English.

The invention relates to an isolated specific binding member (I) which recognizes an epidermal growth factor receptor (EGFR) epitope which is found in tumourigenic, hyperproliferative or abnormal cells and not detectable in normal cells. The EGFR epitope is located within the region comprising residues 273-501 of EGFR and does not demonstrate any amino acid sequence alterations or substitutions from normal EGFR. (I) is capable of binding the de2-7 EGFR at an epitope distinct from the junctional peptide and does not bind to EGFR on normal cells in the absence of aberrant expression, or in the absence of amplification of normal wild-type gene. The binding member comprises the VH and VL polypeptide sequence of monoclonal antibody (mAb) 806. (I) is useful for treating or diagnosing human or animal body, especially for treating tumour in a human. (I) is useful for the preparation of a medicament and for preventing or treating cancer which is located in or adjacent the brain, in a mammal. (I) is also useful for detecting the presence of amplified EGFR, de2-7EGFR or EGFR with high mannose glycosylation, where EGFR is measured by contacting a biological sample from a mammal in which the presence of amplified EGFR, de2-7EGFR or EGFR with a high mannose glycosylation is suspected with (I) under conditions that allow binding of the EGFR to the antibody to occur, and detecting whether binding has occurred between the EGFR from the sample and the antibody, where the detection of binding indicates that presence or activity of the EGFR in the sample. This method is useful for detecting cancer in mammals by detecting the presence or activity of an EGFR which indicates the existence of a tumour or cancer in the mammal. A pharmaceutical composition comprising (I), and optionally vehicle, carrier or diluent is useful for preventing and/or treating cancer in mammals, especially for treating brain-resident cancers that produce aberrantly expressed EGFR in mammals, such as glioblastoma, medulloblastoma, meningioma, neoplastic astrocytoma or neoplastic arteriovenous malformations, and malignant neural tumours in mammals. The present sequence represents the mAb 806 VH region

Sequence 134 AA:

PD 23-SEP-2004.  
XX  
PF 12-MAR-2004; 2004WO-JP003334.  
XX  
PR 13-MAR-2003; 2003JP-00067832.  
XX  
PA (CHUS ) CHUGAI SEIYAKU KK.  
XX  
PI Tsuchiya M, Hirata Y;  
XX  
DR WPI; 2004-677525/66.  
DR N-PSDB; ADS14287.  
XX  
PT Novel ligand having agonist activity with respect to variant receptor  
PT e.g., variant thrombopoietin receptor, useful for treating disease  
PT resulting due to variant receptor such as congenital non-megakaryocyte  
PT thrombocytopenia.  
XX  
PS Disclosure; SEQ ID NO 14; 132pp; Japanese.  
XX  
CC The invention relates to a novel ligand (preferably an antibody) (I)  
CC having agonist activity with respect to a variant receptor. A ligand of  
CC the invention has antidiabetic, haemostatic, and endocrine-gen. activity.  
CC The ligand is useful for treating the disease caused due to variant  
CC receptor, which involves combining the ligand/antibody with the variant  
CC receptor, where the disease is congenital non-megakaryocyte  
CC thrombocytopenia. A ligand of the invention is useful for transmitting a  
CC signal to a variant receptor, which involves combining the variant  
CC receptor with the ligand. The invention is useful for treating diseases  
CC resulting due to variant receptor, such as type II diabetes and laron  
CC syndrome. The ligand enables signal transduction function of  
CC thrombopoietin, with respect to variant receptor. The present sequence is  
CC used in the exemplification of the invention.  
XX  
SQ Sequence 519 AA;  
  
Query Match 77.3%; Score 569.5; DB 8; Length 519;  
Best Local Similarity 79.4%; Pred. No. 1.1e-44;  
Matches 108; Conservative 9; Mismatches 14; Indels 5; Gaps 1;  
  
QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLTCSVTGYSITSGYAWNWIRQFP 60  
Db 1 MRVLIPLWLTAFPGILSDVQLQESGPGLVKPSQSLTCTVTGYSITSDYAWNWIRQLP 60  
  
QY 61 GNKLEWMGYISYSGFTSYNPSLSRISRTDTSKNQFFLQLNSVTSEDATYICARWDYG 120  
Db 61 GNKLEWMGYITYSGYSIYNPSLSKRSISRTDTSKNQLFLQLNSVTTEDATYICV----- 115  
  
QY 121 TTYGYFDVWGQGTTVT 136  
Db 116 GGYDNMDYWGQGTSTV 131  
  
RESULT 11  
ADO44274  
ID ADO44274 standard; protein; 120 AA.  
XX  
AC ADO44274;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Consensus sequence of variable heavy chain region of anti-C3-2.  
XX  
KW antibody; anti-C3-2; C3; C3a; C5a; complement activation;  
KW inflammatory disease; kappa light chain.  
XX  
OS Mus sp.  
XX  
PN WO2004031240-A1.  
XX  
PD 15-APR-2004.  
XX  
PF 03-OCT-2003; 2003WO-EP010989.

XX 04-OCT-2002; 2002EP-00447190.  
PR 16-OCT-2002; 2002US-0418947P.  
XX  
PA (INNO-) INNOGENETICS NV.  
PA (SANQ-) SANQUIN BLOOD SUPPLY FOUND AMSTERDAM.  
XX  
PI De Winter H, Buysse M, Hack E;  
XX  
DR WPI; 2004-316465/29.  
XX  
PT New molecule capable of inhibiting complement activation, and which  
PT specifically binds on a functional domain exposed on native human C3,  
PT useful for preventing or treating inflammatory diseases mediated by  
PT activation of complement.  
XX  
PS Example 12; Fig 17; 72pp; English.  
XX  
CC The specification describes a monoclonal antibody, designated anti-C3-2,  
CC which specifically binds on a functional domain exposed on native human  
CC C3, thus inhibiting the generation of the biologically active peptides  
CC such as C3a and C5a. The functional domain is in part located on the 23  
CC kD-a-chain fragment of C3c. The antibody is useful for the preparation of  
CC a medicament for inhibiting complement activation, preferably for  
CC preventing or treating inflammatory diseases mediated by activation of  
CC complement. The present sequence represents the consensus sequence of the  
CC heavy chain variable region of the monoclonal antibody anti-C3-2, derived  
CC from N-terminal sequencing, primer-induced sequence and sequence  
CC confirmed by nested PCR.  
XX  
SQ Sequence 120 AA;  
  
Query Match 75.5%; Score 556.5; DB 8; Length 120;  
Best Local Similarity 89.0%; Pred. No. 3.5e-44;  
Matches 105; Conservative 3; Mismatches 9; Indels 1; Gaps 1;  
  
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSITSGYAWNWIRQFPGNKLEWMGYISYSGFTSY 78  
Db 1 DVQLQESGPGLVKPSQSLTCTVAGYSITSDYAWNWIRQFPGNKLEWMGYISYSGFTSY 60  
  
QY 79 NPSLSRISRTDTSKNQFFLQLNSVTSEDATYICARWDYGTTYGYFDVWGQGTTVT 136  
Db 61 NPSLSRISRTDTSKNQFFLQLNSVTTEDATYICAR-DYDGAYWYFDVWGAGTTVT 117  
  
RESULT 12  
ADO44271  
ID ADO44271 standard; protein; 120 AA.  
XX  
AC ADO44271;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Sequence of variable heavy chain region of the anti-C3-2 antibody.  
XX  
KW antibody; anti-C3-2; C3; C3a; C5a; complement activation;  
KW inflammatory disease; kappa light chain.  
XX  
OS Mus sp.  
XX  
PN WO2004031240-A1.  
XX  
PD 15-APR-2004.  
XX  
PF 03-OCT-2003; 2003WO-EP010989.  
XX  
PR 04-OCT-2002; 2002EP-00447190.  
PR 16-OCT-2002; 2002US-0418947P.  
XX  
PA (INNO-) INNOGENETICS NV.  
PA (SANQ-) SANQUIN BLOOD SUPPLY FOUND AMSTERDAM.  
XX  
PI De Winter H, Buysse M, Hack E;



XX WPI; 2004-316465/29.  
DR N-PSDB; ADO44270.  
XX New molecule capable of inhibiting complement activation, and which  
PT specifically binds on a functional domain exposed on native human C3,  
PT useful for preventing or treating inflammatory diseases mediated by  
PT activation of complement.  
XX  
PS Disclosure; Fig 14B; 72pp; English.  
XX  
CC The specification describes a monoclonal antibody, designated anti-C3-2,  
CC which specifically binds on a functional domain exposed on native human  
CC C3, thus inhibiting the generation of the biologically active peptides  
CC such as C3a and C5a. The functional domain is in part located on the 23  
CC kD-a-chain fragment of C3c. The antibody is useful for the preparation of  
CC a medicament for inhibiting complement activation, preferably for  
CC preventing or treating inflammatory diseases mediated by activation of  
CC complement. The present sequence represents the heavy chain region of the  
CC monoclonal antibody anti-C3-2.  
XX  
SQ Sequence 120 AA;

Query Match 75.5%; Score 556.5; DB 8; Length 120;  
Best Local Similarity 89.0%; Pred. No. 3.5e-44;  
Matches 105; Conservative 3; Mismatches 9; Indels 1; Gaps 1;  
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYISITSGYAWNWIQFPGNKLEWMGYISYSGFTSY 78  
Db 1 DVQLQESGPGLVKPSQSLTCTVAGYSITSDYAWNWIQFPGNKLEWMGYISYSGSTSY 60  
QY 79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTYYGYFDVWGQTTVT 136  
Db 61 NPSLKSRIISITRDTSKNQFFLQLNSVTTEDTATYYCAR-DYDGAYWYFDVWGAGTTVT 117

RESULT 13  
ADJ76886  
ID ADJ76886 standard; protein; 127 AA.  
XX  
AC ADJ76886;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Anti-IGF-1R related protein #4.  
XX  
KW cytotstatic; antipsoriatic; antibody;  
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;  
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;  
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;  
KW CDR.  
XX  
OS Mus musculus.  
XX  
PN WO2003059951-A2.  
XX  
PD 24-JUL-2003.  
XX  
PF 20-JAN-2003; 2003WO-FR000178.  
XX  
PR 18-JAN-2002; 2002FR-00000653.  
PR 18-JAN-2002; 2002FR-00000654.  
PR 07-MAY-2002; 2002FR-00005753.  
XX  
PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
XX  
PI Goetsch L, Corvaia N, Leger O;  
XX  
DR WPI; 2003-569653/53.  
XX  
PT New antibodies that bind to human insulin-like growth factor receptor,  
PT useful for treatment, prevention and diagnosis of cancers.  
XX

PS Disclosure; SEQ ID NO 52; 164pp; French.  
XX  
CC The invention relates to an isolated antibody (Ab), and its functional  
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-  
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth  
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine  
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or  
CC treat diseases associated with overexpression and/or abnormal activity of  
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with  
CC hyperactivity of signal transduction pathways mediated by interaction of  
CC these receptors with their ligands. Especially they inhibit  
CC transformation of normal cells to tumor cells, inhibit growth and/or  
CC proliferation of tumor cells, so are useful against cancers of the  
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and  
CC also for treating psoriasis. Ab are also used to diagnose diseases caused  
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a  
XX protein sequence used to generate the Ab of the invention.  
SQ Sequence 127 AA;

Query Match 75.2%; Score 554; DB 7; Length 127;  
Best Local Similarity 82.0%; Pred. No. 6.5e-44;  
Matches 105; Conservative 6; Mismatches 13; Indels 4; Gaps 2;  
QY 9 LFTAFPGILSDVQLQESGPGLVKPSQSLTCSVTGYISITSGYAWNWIQFPGNKLEWMG 68  
Db 1 LLTAIPGILSDVQLQESGPGLVKPSQSLTCSVTGYISITGGYLNWIQFPGNKLEWMG 60  
QY 69 YISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTYYGYFDV 128  
Db 61 YISYDGTNNYKPSLKDRIISITRDTSKNQFFLKLNSVTNEDTATYYCAR--YGRV--FFDY 116  
QY 129 WGQGTTVT 136  
Db 117 WGQGTTLT 124

RESULT 14  
ADZ67056  
ID ADZ67056 standard; protein; 127 AA.  
XX  
AC ADZ67056;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.  
XX  
KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;  
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;  
KW musculoskeletal disease; respiratory disease; lung tumor;  
KW endocrine disease; gynecology and obstetrics; breast tumor;  
KW endometroid carcinoma; gastrointestinal disease; colon tumor;  
KW antipsoriatic; psoriasis; dermatological disease; immune disorder;  
KW immunoglobulin; heavy chain variable region.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..10 /note= "leader peptide"  
FT Region 41..46 /note= "CDR1"  
FT Region 61..76 /note= "CDR2"  
FT Region 109..116 /note= "CDR3"  
XX  
PN US2005084906-A1.  
XX  
PD 21-APR-2005.  
XX  
PF 16-DEC-2003; 2003US-00735916.  
XX







GenCore version 5.1.8  
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One protein - protein search, using sw model

Run on: May 19, 2006, 17:40:37 ; Search time 25.9048 Seconds  
(without alignments)  
505.138 Million cell updates/sec

Title: US-09-889-936A-6  
Perfect score: 737  
Sequence: 1 MRVLILLWLFTAFPGILSDV.....WDYGTTYGYFDVWGQGTTVT 136

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605.5	82.2	135	2 PL0100	Ig heavy chain pre
2	587.5	79.7	134	2 B24672	Ig heavy chain pre
3	579	78.6	149	2 S30752	Ig heavy chain pre
4	561	76.1	137	1 AVMS35	Ig heavy chain pre
5	557	75.6	116	1 HVMS1B	Ig heavy chain pre
6	555.5	75.4	136	2 S07637	Ig heavy chain v r
7	539	73.1	116	1 HVMS1	Ig heavy chain pre
8	525.5	71.3	116	2 S38718	Ig heavy chain v r
9	524	71.1	121	2 S37200	Ig heavy chain v r
10	522	70.8	117	2 I28195	Ig heavy chain v r
11	509	69.1	119	2 C53285	Ig heavy chain v a
12	508.5	69.0	114	2 T01262	Ig heavy chain v r
13	504	68.4	119	2 E25114	Ig heavy chain v r
14	498.5	67.6	115	2 D33932	Ig mu chain precu
15	494	67.0	115	2 F25114	Ig heavy chain v r
16	487	66.1	119	2 C25114	Ig heavy chain v r
17	484.5	65.7	120	2 A25114	Ig heavy chain v r
18	476.5	64.7	117	1 HVMS73	Ig heavy chain pre
19	469	63.6	123	2 S42771	Ig heavy chain - m
20	466	63.2	106	2 S59639	Ig heavy chain v r
21	464.5	63.0	100	2 S14485	Ig heavy chain v r
22	463	62.8	119	2 D25114	Ig heavy chain v r
23	462.5	62.8	106	2 S26464	Ig heavy chain v r
24	461	62.6	117	2 I57810	gene C72-3A1 prote
25	455.5	61.8	104	2 S26467	Ig heavy chain v r
26	451	61.2	113	1 G2MS60	Ig heavy chain v r
27	441.5	59.9	102	2 S14488	Ig heavy chain v r
28	437	59.3	111	2 S13687	Ig heavy chain v r
29	437	59.3	140	2 I37782	Ig variable region

30	436.5	59.2	101	2 S14484	Ig heavy chain v r
31	435	59.0	112	2 S13685	Ig heavy chain v r
32	432	58.6	112	2 S13686	Ig heavy chain v r
33	427.5	58.0	102	2 S14487	Ig heavy chain v r
34	427	57.9	102	2 S14486	Ig heavy chain v r
35	426	57.8	110	2 S13688	Ig heavy chain v r
36	417	56.6	130	2 S31690	Ig heavy chain v r
37	416	56.4	123	2 S30530	Ig heavy chain v r
38	415.5	56.4	155	2 S31511	Ig heavy chain - h
39	414.5	56.2	94	2 S26461	Ig heavy chain v r
40	411.5	55.8	139	2 S31586	Ig heavy chain v r
41	409.5	55.6	155	2 S31512	Ig heavy chain - h
42	406	55.1	146	2 S09711	Ig heavy chain v r
43	402.5	54.6	137	2 S31676	Ig heavy chain v r
44	400	54.3	147	2 S13519	Ig heavy chain v r
45	397.5	53.9	145	2 S78055	Ig heavy chain pre

ALIGNMENTS

RESULT 1

PL0100

Ig heavy chain precursor V region (40-140) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 23-Jul-1999

C;Accession: PL0100

R;Near, R.I.; Haber, E.

Mol. Immunol. 26, 371-382, 1989

A;Title: Characterization of the heavy and light chain immunoglobulin variable region ger

A;Reference number: PL0100; MUID:89238344; PMID:2497340

A;Accession: PL0100

A;Molecule type: DNA

A;Residues: 1-135 <NEA>

A;Cross-references: UNIPARC:UPI0000114EA6; GB:M27660; NID:g341745; PIDN:AAA58746.1; PID:s

A;Experimental source: strain A/J

A;Note: the VH40-140 gene segment is classified as a member of the 36-60 VH gene family

C;Genetics:

A;Introns: 15/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-115/Domain: V segment #status predicted <VRE>

F;33-116/Domain: immunoglobulin homology <IMM>

F;117-118/Domain: D segment #status predicted <DRE>

F;119-135/Domain: J segment #status predicted <JRE>

Query Match 82.2%; Score 605.5; DB 2; Length 135;  
Best Local Similarity 82.4%; Pred. No. 2.6e-45;  
Matches 112; Conservative 12; Mismatches 7; Indels 5; Gaps 1;

Qy	1	MRVLILLWLFTAFPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTITGYAWNWIQFP	60
Db	1	MRVLILLWLFTAFPGGLSDVQLQESGPGLVKPSQSLTCTVTGYSTITSDYAWSWIRQFP	60

Qy	61	GNKLEWMGYISYSGFTSYNPSILRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWDYG	120
		:     : : :     : : :	
Db	61	GNRLEWMGYITYNGYTTYNPISLKSFRFSITRDTSKNQLFQLSSVTEDATYYCAR----	116

Qy	121	TTYGYFDVWGQGTTVT	136
		:	
Db	117	-SYDYFDYWGQGTTLT	131

RESULT 2

B24672

Ig heavy chain precursor V region (VGAM3-2) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 18-Oct-1996

C;Accession: B24672

R;Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A;Reference number: A91022; MUID:860555722; PMID:2998759



QY 121 TTYGYFDWVGQGT T 136  
120 HLY-YFDYWGQGT T 134

## RESULTS

HVMS1B  
Ig heavy chain precursor V region (1B43) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C/Accession: JT0508  
R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A/Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A/Reference number: JT0501; MUID:89279149; PMID:2499654  
A/Accession: JT0508  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-116 <LEV>  
A/Cross-references: UNIPROT:P18532; UNIPARC:UPI000000278E1  
A/Experimental source: strain BALB/cJ  
A/Note: this sequence belongs to the VH3660 subfamily  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-116/Product: Ig heavy chain V region (1B43) #status predicted <MAT>  
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 75.6%; Score 557; DB 1; Length 116;  
Best Local Similarity 91.4%; Pred. NO. 3.3e-41;  
Matches 106; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy	1 MRVLILLWLFAPPGILSDVOLQESGPLVKPSQSLSLTCSVTGYSTSGYAWNWIROFF 60 
Db	1 MRVLIILCLFAPPGILSDVOLESGPDLVKPSQSLSLTCTVTGYSTSGYSWHIWIROFF 60 

[illegible]

## RESULT 6

S07637  
Ig heavy chain V region (PTF.02) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 23-Jul-1999  
C:Accession: S07637  
R:Urakov, D.N.; Deev, S.M.; Polyakov, O.L.  
Nucleic Acids Res. 17, 9481, 1989  
A:Title: The structure of the expressible VH gene from a hybridoma producing monoclonal  
A:Reference number: S07637; MUID:90067954; PMID:2587273  
A:Accession: S07637  
A:Molecule type: DNA  
A:Residues: 1-136 <URA>  
A:Cross-references: UNIPARC:UPI0000115E36; EMBL:X16740; NID:g52099; PIDN:CAA34714.1; PID  
A:Note: the authors translated the codon TAT for residue 112 as Ile, TAC for residue 113  
C:Genetics:  
A:Introns: 15/3  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:33-116/Domain: immunoglobulin homology <IMM>

Query Match	75.4%	Score 555.5;	DB 2;	Length 136;
Best Local Similarity	77.9%;	Pred. No. 5.2e-41;		
Matches 106;	Conservative	9;	Mismatches 18;	Indels 3;
				Gaps 1;

<b>Qy</b>	1	MRVLILLWLF	AFFPGILSDVQLQESGGLVKPQSLSLTCSVTGYSITSGYAWNWIROFP	60
		: : :	: : :	:
<b>D<sub>b</sub></b>	1	MKVLSLLYLLTAIPGILSTVOLQESGGLVKPQSLSLTCSVTDFISITGYVWHWIROFP	60	

[illegible]





C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
Query Match 68.4%; Score 504; DB 2; Length 119;  
Best Local Similarity 81.5%; Pred. No. 1.2e-36;  
Matches 97; Conservative 5; Mismatches 13; Indels 4; Gaps 2;  
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYISITSGYAWNWIROPFGNKLEWMGYISYSGFTSY 78  
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYISITSGYYWNWIRPFGNKLEWMGYISYDGSNHY 60  
QY 79 NPSLRSRISFTRDTSKNQFFLQNSVTSEDTATYYCAR---WDYGTITYGY-FDVMGQGT 133  
Db 61 NPSLKNRISITRDTSKNQFFLKLNSVTIEDTATYYCARPLYRYRDEEYYAMDYWGQGT 119  
RESULT 14  
D33932  
Ig mu chain precursor V region (E7) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 23-May-1997  
C;Accession: D33932  
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989  
A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-l  
A;Reference number: A33932; MUID:89282823; PMID:2499887  
A;Accession: D33932  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-115 <BAC>  
A;Cross-references: UNIPARC:UPI00001768F1; GB:M27106  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;33-115/Domain: immunoglobulin homology <IMM>  
Query Match 67.6%; Score 498.5; DB 2; Length 115;  
Best Local Similarity 83.6%; Pred. No. 3.5e-36;  
Matches 97; Conservative 9; Mismatches 9; Indels 1; Gaps 1;  
QY 1 MRVLILLWLFTAPPGILSDVQLQESGPGLVKPSQSLTCSVTGYISITSGYAWNWIROPF 60  
Db 1 MMVLSLLYLLTALPGILSEVQLQESGPGSLVKPSQTLTCSVTGDSITSGY-WNWIRKFP 59  
QY 61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQNSVTSEDTATYYCAR 116  
Db 60 GNKLEYMGYISYSGSTYYNPSLSKRSISITRDTSKNQYLLQNSVTEDTATYYCAR 115  
RESULT 15  
F25114  
Ig heavy chain V region (HP12) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 20-Jun-2000  
C;Accession: F25114  
R;Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.  
EMBO J. 4, 3681-3688, 1985  
A;Title: The idiotypic network and the internal image: possible regulation of a germ-lin  
A;Reference number: A91028; MUID:86136012; PMID:3937730  
A;Accession: F25114  
A;Molecule type: mRNA  
A;Residues: 1-115 <OLL>  
A;Cross-references: UNIPARC:UPI0000115D28; GB:X03379; NID:g52013; PIDN:CAA27101.1; PID:9  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
Query Match 67.0%; Score 494; DB 2; Length 115;  
Best Local Similarity 79.1%; Pred. No. 8.6e-36;  
Matches 91; Conservative 8; Mismatches 16; Indels 0; Gaps 0;  
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYISITSGYAWNWIROPFGNKLEWMGYISYSGFTSY 78  
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYISITSGYYWNWIRPFGDKLEWMGFIRYDGSNNY 60

Qy 79 NPSLRSRISFTRDTSKNQFFLQNSVTSEDTATYYCARWDYGTITYGYFDVMGQGT 133  
Db 61 NPSLKNRISITRDTSKNQFFLRLNSVTTEDTATYYCAVFGYDMDYYAMDYWGQGT 115

Search completed: May 19, 2006, 17:47:23  
Job time : 26.9048 secs





GenCore version 5.1.8  
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On-line protein - protein search, using sw model

Run on: May 19, 2006, 17:34:57 ; Search time 207.238 Seconds  
(without alignments)  
607.041 Million cell updates/sec

Title: US-09-889-936A-6  
Perfect score: 737  
Sequence: 1 MRVLILLWLFTAPPGILSDV.....WDYGTTYGYFDVWGQTTVT 136

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609.5	82.7	483	Q5U413_MOUSE	Q5u413 mus musculus
2	568	77.1	479	Q99M22_MOUSE	Q99m22 mus musculus
3	561	76.1	137	HV46_MOUSE	P01822 mus musculus
4	561	76.1	615	Q569B6_RAT	Q569b6 rattus norv
5	557	75.6	116	HV61_MOUSE	P18532 mus musculus
6	555.5	75.4	136	Q6LBQ5_MOUSE	Q6lbq5 mus musculus
7	548	74.4	590	Q569B8_RAT	Q569b8 rattus norv
8	539	73.1	116	HV60_MOUSE	P18531 mus musculus
9	504	68.4	119	Q53VQ5_MOUSE	Q53vq5 mus musculus
10	494	67.0	115	Q53VQ1_MOUSE	Q53vq1 mus musculus
11	487	66.1	119	Q53VR3_MOUSE	Q53vr3 mus musculus
12	484.5	65.7	120	Q53VR7_MOUSE	Q53vr7 mus musculus
13	476.5	64.7	117	HV62_MOUSE	P18533 mus musculus
14	473	64.2	98	Q53VQ4_MOUSE	Q53vq4 mus musculus
15	463	62.8	119	Q53VQ9_MOUSE	Q53vq9 mus musculus
16	462	62.7	98	Q53VR2_MOUSE	Q53vr2 mus musculus
17	458	62.1	98	Q53VR6_MOUSE	Q53vr6 mus musculus
18	453	61.5	98	Q53VQ0_MOUSE	Q53vq0 mus musculus
19	451	61.2	113	HV47_MOUSE	P01823 mus musculus
20	450	61.1	262	Q65Z11_MOUSE	Q65zi1 mus musculus
21	443	60.1	98	Q53VQ8_MOUSE	Q53vq8 mus musculus
22	428.5	58.1	478	Q7Z379_HUMAN	Q7z379 homo sapien
23	423.5	57.5	477	Q6GMX7_HUMAN	Q6gmx7 homo sapien
24	420	57.0	476	Q6GMX1_HUMAN	Q6gmx1 homo sapien
25	403.5	54.7	465	Q6GMX6_HUMAN	Q6gmx6 homo sapien
26	399.5	54.2	576	Q6P418_HUMAN	Q6p418 homo sapien
27	397.5	53.9	477	Q5I0J1_RAT	Q5i0j1 rattus norv
28	395	53.6	591	Q5I0L9_RAT	P01819 rattus norv
29	392.5	53.3	144	HV43_MOUSE	P01819 mus musculus
30	392	53.2	478	Q6NYH3_HUMAN	Q6nyh3 homo sapien
31	389.5	52.8	469	Q5M839_RAT	Q5m839 rattus norv

32	387	52.5	119	2	Q9UL73_HUMAN	Q9ul73 homo sapien
33	386.5	52.4	146	1	HV21_HUMAN	P06331 homo sapien
34	386.5	52.4	458	2	Q5M842_RAT	Q5m842 rattus norv
35	382.5	51.9	492	2	Q7Z374_HUMAN	Q7z374 homo sapien
36	382	51.8	139	2	Q86SX2_HUMAN	Q86sx2 homo sapien
37	381.5	51.8	620	2	Q96EY0_HUMAN	Q96ey0 homo sapien
38	374.5	50.8	496	2	Q96KX8_HUMAN	Q96kx8 homo sapien
39	372.5	50.5	150	2	Q95973_HUMAN	Q95973 homo sapien
40	370	50.2	597	2	Q9BQB8_HUMAN	Q9bqb8 homo sapien
41	369	50.1	482	2	Q91X92_MOUSE	Q91x92 mus musculu
42	368	49.9	595	2	Q8WUX4_HUMAN	Q8wux4 homo sapien
43	368	49.9	597	2	Q6GMX5_HUMAN	Q6gmx5 homo sapien
44	368	49.9	597	2	Q9BU10_HUMAN	Q9bul0 homo sapien
45	368	49.9	625	2	Q96AA6_HUMAN	Q96aa6 homo sapien

ALIGNMENTS

RESULT 1  
Q5U413\_MOUSE  
ID Q5U413\_MOUSE PRELIMINARY; PRT; 483 AA.  
AC Q5U413;  
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.  
DT 07-DEC-2004, sequence version 1.  
DT 07-FEB-2006, entry version 18.  
DE LOC544903 protein.  
GN Name=LOC544903;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
NUCLEOTIDE SEQUENCE.  
STRAIN=FVB/N; TISSUE=Colon;  
NIH MGC Project;  
Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
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EMBL; BC085312; AAH85312.1; -; mRNA.  
Ensembl; ENSMUSG00000054328; Mus musculus.  
InterPro; IPR003599; Ig.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003597; Ig\_cl.  
InterPro; IPR003006; Ig\_MHC.  
InterPro; IPR003596; Ig\_v.



RT "Amino-acid sequence of the variable region of the heavy (alpha) chain  
of a mouse myeloma protein with anti-hapten activity.";   
Rf Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).   
RN [5]   
IP SEQUENCE REVISION TO 53.   
RX MEDLINE=77244979; PubMed=268248;   
RA Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;   
RT "Model-building studies of antigen-binding sites: the hapten-binding   
site of mopc-315.";   
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).   
CC -!- MISCELLANEOUS: This alpha chain was isolated from a myeloma   
CC protein that has anti-dinitrophenyl activity.   
CC -----   
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CC -----   
DR EMBL; M27638; AAA61337.1; -; Genomic\_DNA.   
DR EMBL; X07880; CAA30727.1; -; Genomic\_DNA.   
DR PIR; PL0102; AVMS35.   
DR HSSP; P01820; 1G7J.   
DR SMR; P01822; 20-137.   
DR Ensembl; ENSMUSG0000057048; Mus musculus.   
DR InterPro; IPR003599; Ig.   
DR InterPro; IPR007110; Ig-like.   
DR InterPro; IPR003596; Ig\_v.   
DR InterPro; IPR013106; V-set.   
DR Pfam; PF07686; V-set; 1.   
DR SMART; SM00409; IG; 1.   
DR SMART; SM00406; IGV; 1.   
DR PROSITE; PS50835; IG\_LIKE; 1.   
KW Direct protein sequencing; Immunoglobulin domain;   
KW Immunoglobulin V region; Signal.   
FT SIGNAL 1 18   
FT CHAIN 19 137 Ig heavy chain V region MOPC 315.   
FT /FTId=PRO\_0000015232.   
FT Framework-1.   
FT REGION 19 48 Complementarity-determining-1.   
FT REGION 49 54 Framework-2.   
FT REGION 55 68 Complementarity-determining-2.   
FT REGION 69 84 Framework-3.   
FT REGION 85 116 Complementarity-determining-3.   
FT REGION 117 126 Framework-4.   
FT REGION 127 137 By similarity.   
FT DISULFID 40 114 G -> GG (in Ref. 1; CAA30727).   
FT CONFLICT 15 15 G -> H (in Ref. 2).   
FT CONFLICT 15 15 GY -> YG (in Ref. 4).   
FT CONFLICT 77 78 N -> D (in Ref. 4).   
FT CONFLICT 102 102 Missing (in Ref. 4).   
FT CONFLICT 123 123   
FT NON TER 137 137   
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;   
  
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Best Local Similarity 77.9%; Pred. No. 3e-46;   
Matches 106; Conservative 12; Mismatches 16; Indels 2; Gaps 2;   
  
QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSTITSGYAMNWIQFP 60  
Db 1 MKVLSLLYLLTAIPGIMSDVQLQESGPGLVKPSQSLSLTCSVTGYSTITSGYFWNWIQFP 60  
  
QY 61 GNKLEWMGYISYSGFTSYNPSLRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYG 120  
Db 61 GNKLEWLGFIKYDGSNGYNPSLKNRVSITRDTSENQFFLKLNSVTEDATYYCA-GDND 119  
  
QY 121 TTYGYFDVWGQGTIVT 136  
Db 120 HLY-YFDYWGQGTTLT 134  
  
RESULT 4  
Q569B6\_RAT PRELIMINARY; PRT; 615 AA.  
AC Q569B6;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.

DT 10-MAY-2005, sequence version 1.   
DT 07-FEB-2006, entry version 12.   
DE LOC314509 protein.   
GN Name=LOC314509;   
OS Rattus norvegicus (Rat).   
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;   
OC Muroidae; Muridae; Murinae; Rattus.   
OX NCBI\_TaxID=10116;   
RN [1]   
RP NUCLEOTIDE SEQUENCE.   
RC TISSUE=Spleen;   
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;   
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,   
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,   
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,   
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,   
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,   
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,   
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,   
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,   
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,   
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,   
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,   
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,   
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,   
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,   
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,   
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,   
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;   
RT "Generation and initial analysis of more than 15,000 full-length human   
and mouse cDNA sequences.";   
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).   
RN [2]   
RP NUCLEOTIDE SEQUENCE.   
RC TISSUE=Spleen;   
RG NIH MGC Project;   
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.   
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CC Distributed under the Creative Commons Attribution-NoDerivs License   
CC -----   
CC EMBL; BC092582; AAH92582.1; -; mRNA.   
DR InterPro; IPR003599; Ig.   
DR InterPro; IPR007110; Ig-like.   
DR InterPro; IPR003597; Ig\_cl.   
DR InterPro; IPR003006; Ig\_MHC.   
DR InterPro; IPR003596; Ig\_v.   
DR InterPro; IPR013106; V-set.   
DR Pfam; PF07654; C1-set; 4.   
DR SMART; SM00409; IG; 1.   
DR SMART; SM00407; IGcl; 2.   
DR SMART; SM00406; IGV; 1.   
DR PROSITE; PS50835; IG\_LIKE; 5.   
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.   
SQ SEQUENCE 615 AA; 67986 MW; BE5C2483C69F186C CRC64;   
  
Query Match 76.1%; Score 561; DB 2; Length 615;   
Best Local Similarity 80.3%; Pred. No. 1.6e-45;   
Matches 110; Conservative 8; Mismatches 17; Indels 2; Gaps 2;   
  
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Db 1 MRTLGLLYLLTALPGILSEVQLQESGPGLVKPSQSLSLTCSVTGYSTITSNY-WGWIRKFP 59  
  
QY 61 GNKLEWMGYISYSGFTSYNPSLRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYG 120  
Db 60 GNKMEWIGHISYSGSTSYNPSLKSRISTRDTSKNQFFLQNSVTEDATYYCARCHGG 119  
  
QY 121 TTYG-YFDVWGQGTIVT 136  
Db 120 PLTGRYFDYWGQGMVT 136



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RESULT 5
HV61_MOUSE
ID HV61_MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 07-MAR-2006, entry version 44.
DE Ig heavy chain V region 1B43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
CC -----
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CC -----
CC PIR; J0508; HVMS1B.
DR PDB; 1KCS; X-ray; H=25-116.
DR PDB; 1KCV; X-ray; H=25-116.
DR Ensembl; ENSMUSG0000061612; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116
FT REGION 19 48
FT REGION 49 53
FT REGION 54 67
FT REGION 68 84
FT REGION 85 116
FT DISULFID 40 114
FT NON TER 116 116
FT STRAND 21 25
FT STRAND 28 30
FT TURN 32 33
FT STRAND 34 34
FT STRAND 36 45
FT TURN 47 49
FT STRAND 50 58
FT TURN 60 61
FT STRAND 64 71
FT TURN 72 73
FT STRAND 74 74
FT STRAND 76 78
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FT TURN 92 95
FT STRAND 96 101
FT STRAND 103 103
FT HELIX 106 108
FT STRAND 110 116
FT SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;
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Query Match 75.6%; Score 557; DB 1; Length 116;  
Best Local Similarity 91.4%; Pred. No. 6.1e-46;  
Matches 106; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY 1 MRVLILLWLTAFPGILSDVQLQESGGLVKPSQSLTCSVTGYSTGYAWNWIQQFP 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MRVLILLCLFTAFPGILSDVQLQESGPDLVKPSQSLTCTVTGYSTGYSHWIQQFP 60

QY 61 GNKLEWGMGYSYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCAR 116
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GNKLEWGMGIHYSGNTSYNPSLKSRISTRDTSKNQFFLQLNSVTTEDATYYCAR 116

RESULT 6
Q6LBQ5_MOUSE
ID Q6LBQ5_MOUSE PRELIMINARY; PRT; 136 AA.
AC Q6LBQ5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE VH gene product (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90067954; PubMed=2587273;
RA Urakov D.N., Deev S.M., Polyanovsky O.L.;
RT "The structure of the expressible VH gene from a hybridoma producing
RT monoclonal antibodies against porcine transferrin.";
RL Nucleic Acids Res. 17:9481-9481(1989).
CC -----
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CC -----
DR EMBL; X16740; CAA34714.1; -; Genomic_DNA.
DR HSSP; P18532; 1KCV.
DR SMR; Q6LBQ5; 20-136.
DR Ensembl; ENSMUSG0000057048; Mus musculus.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON TER 1 1
SQ SEQUENCE 136 AA; 15307 MW; 5B0F439CCFB15C3A CRC64;

Query Match 75.4%; Score 555.5; DB 2; Length 136;
Best Local Similarity 77.9%; Pred. No. 1e-45;
Matches 106; Conservative 9; Mismatches 18; Indels 3; Gaps 1;

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QY 61 GNKLEWGMGYSYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWDYG 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GNKLEWGMGIYDGSNGYNPSLKNRISITRDTSKNQFFLQLNSVTTEDATYYCTR---G 117

QY 121 TTYGYFDVWGQGTIVT 136
Db | : | | | | | |
118 DGYHFFTYWGQGLVT 133

RESULT 7
Q569B8_RAT
ID Q569B8_RAT PRELIMINARY; PRT; 590 AA.
AC Q569B8;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE RGD1359202 protein.
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GN. Name=RGD1359202;
QS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1].
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2].
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC092580; AAH92580.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 590 AA; 65088 MW; FAC77FFA82302304 CRC64;

Query Match 74.4%; Score 548; DB 2; Length 590;
Best Local Similarity 78.4%; Pred. No. 2.7e-44;
Matches 105; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

Qy 3 VLILLWLTAFPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIQFPGN 62
Db 1 MLVLLYLLTALPGILSEVQLQESGPGLVKPSQSLTCSVTGYSTITSSYRWNWIRKFPGN 60

Qy 63 KLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWDYGT 122
Db 61 KLEWMGYINSAGSTNYNPSLSKRSISITRDTSKNQFFLQLNSVTTEDATYYCARESPSTR 120

Qy 123 YGYFDVWGQGTIVT 136
Db 121 --RFAYWGQGLTVT 132

RESULT 8
HV60_MOUSE
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ID HV60_MOUSE STANDARD; PRT; 116 AA.
AC P18531;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1].
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
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CC -----
DR PIR; JT0509; HVMS31.
DR PDB; 1EZV; X-ray; X=20-116.
DR Ensembl; ENSMUSG00000057048; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116
FT -----
FT REGION 19 48
FT REGION 49 53
FT REGION 54 67
FT REGION 68 84
FT REGION 85 116
FT DISULFID 40 114
FT NON_TER 116 116
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FT HELIX 106 108
SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 73.1%; Score 539; DB 1; Length 116;
Best Local Similarity 87.1%; Pred. No. 3.4e-44;
Matches 101; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIQFPP 60
Db 1 MKVLSLLYLLTALPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIQFPP 60

Qy 61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCAR 116
Db 61 GNKLEWMGYISYDGSNNYNSPLKNRISITRDTSKNQFFLKLNSVTTEDATYYCAR 116
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RESULT 9  
Q53VQ5 MOUSE  
ID Q53VQ5\_MOUSE PRELIMINARY; PRT; 119 AA.  
AC Q53VQ5;  
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 24-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE VH-D-JH region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86136012; PubMed=3937730;  
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;  
RT "The idiotypic network and the internal image: possible regulation of  
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
antibodies in the GAT system.";  
RL EMBO J. 4:3681-3688(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 28-29.  
RX Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.  
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DR EMBL; X03378; CAA27095.1; -; mRNA.  
DR SMR; Q53VQ5; 1-119.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
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DR SMART; SM00406; IGV; 1.  
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Query Match 68.4%; Score 504; DB 2; Length 119;  
Best Local Similarity 81.5%; Pred. No. 8.5e-41;  
Matches 97; Conservative 5; Mismatches 13; Indels 4; Gaps 2;  
  
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QY 79 NPSLRSRISFTSDTSKNQFFLQNSVTSEDATYYCAR---WDYGTITYGY-FDVMGQGT 133  
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AC Q53VQ1;  
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 24-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE VH-D-JH region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86136012; PubMed=3937730;  
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;  
RT "The idiotypic network and the internal image: possible regulation of  
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
antibodies in the GAT system.";  
RL EMBO J. 4:3681-3688(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 28-29.  
RX Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.  
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DR EMBL; X03376; CAA27083.1; -; mRNA.  
DR SMR; Q53VR3; 1-119.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.

"The idiotypic network and the internal image: possible regulation of  
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
antibodies in the GAT system.";  
RL EMBO J. 4:3681-3688(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 28-29.  
RX Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.  
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FT NON\_TER 1  
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Matches 91; Conservative 8; Mismatches 16; Indels 0; Gaps 0;  
  
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QY 79 NPSLRSRISFTSDTSKNQFFLQNSVTSEDATYYCARWDYGTITYGYFDVMGQGT 133  
Db 61 NPSLKRISITRDTSKNQFFLRLNSVTEDATYYCAVFGYDMDYVAMDYWGQGT 115  
  
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AC Q53VR3;  
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 24-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE VH-D-JH region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86136012; PubMed=3937730;  
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;  
RT "The idiotypic network and the internal image: possible regulation of  
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
antibodies in the GAT system.";  
RL EMBO J. 4:3681-3688(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 28-29.  
RX Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.  
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QY 79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWDY----GTTYGYFDVWGQGT 133  
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AC Q53VR7;  
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 24-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE VH-D-JH region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Murioidea; Muridae; Murinae; Mus.  
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RN [1]  
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RX MEDLINE=86136012; PubMed=3937730;  
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;  
RT "The idiotypic network and the internal image: possible regulation of  
RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)  
RT antibodies in the GAT system.";  
RL EMBO J. 4:3681-3688(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 28-29.  
RA Fougereau M.;  
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; X03374; CAA27071.1; -; mRNA.  
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DR InterPro; IPR003599; Ig.  
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DR SMART; SM00406; IGv; 1.  
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Matches 91; Conservative 8; Mismatches 16; Indels 5; Gaps 1;  
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Dd 1 DVHLQESGPGLVKPSQSLSLTCSVTGYSITRGYNWNWIRRFPGNKLEWMGYINYDGSNNY 60  
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AC P18533;  
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DT 01-NOV-1990, sequence version 1.  
DT 07-MAR-2006, entry version 37.  
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Murioidea; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BALB/cJ;  
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;  
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
RT "Early onset of somatic mutation in immunoglobulin VH genes during the  
RT primary immune response.";  
RL J. Exp. Med. 169:2007-2019(1989).  
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
CC -----  
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CC -----  
DR PIR; JT0510; HVMS73.  
DR HSSP; P01820; IG7J.  
DR SMR; P18533; 19-117.  
DR Ensembl; ENSMUSG0000059520; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
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DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
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FT Ig-like.  
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FT By similarity.  
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Query Match 64.7%; Score 476.5; DB 1; Length 117;  
Best Local Similarity 75.2%; Pred. No. 3.9e-38;  
Matches 88; Conservative 15; Mismatches 13; Indels 1; Gaps 1;  
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Dd 1 MKMFTLLYLLTVVPGILSDVQLQESGPGLVKPSQSIALTCTVTGISTTGNRWWSWIRQF 60  
QY 60 PGNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCAR 116  
Dd 61 PGNKLEWIGYIYSAITSYNPSPKSRTTITRDTSKNQFFLEMNSLTAEDTATYYCAR 117  
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ID Q53VQ4\_MOUSE PRELIMINARY; PRT; 98 AA.  
AC Q53VQ4;  
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 24-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE VH region (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Murioidea; Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;





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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:46:56 ; Search time 39.3968 Seconds  
(without alignments)  
302.161 Million cell updates/sec

Title: US-09-889-936A-6  
Perfect score: 737  
Sequence: 1 MRVLILLWLTAFPGILSDV.....WDYGTTYGYFDVWGQGTTVT 136

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB.pep.\*  
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6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pep.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	588	79.8	137	1	US-08-137-117D-31 Sequence 31, Appl
2	588	79.8	137	1	US-08-436-717-31 Sequence 31, Appl
3	541	73.4	119	2	US-08-767-128-18 Sequence 18, Appl
4	525.5	71.3	117	1	US-08-308-494A-13 Sequence 13, Appl
5	514	69.7	118	2	US-09-065-059-11 Sequence 11, Appl
6	514	69.7	118	2	US-08-913-555-11 Sequence 11, Appl
7	510.5	69.3	114	1	US-08-111-080-23 Sequence 23, Appl
8	510.5	69.3	114	1	US-08-211-980-23 Sequence 23, Appl
9	510.5	69.3	114	5	PCT-US93-07967-23 Sequence 23, Appl
10	509.5	69.1	137	2	US-08-466-151-7 Sequence 7, Appl
11	509.5	69.1	137	2	US-08-466-163B-7 Sequence 7, Appl
12	509.5	69.1	137	2	US-09-802-096-7 Sequence 7, Appl
13	509.5	69.1	137	2	US-09-802-077-7 Sequence 7, Appl
14	509.5	69.1	137	2	US-09-925-179-7 Sequence 7, Appl
15	509	69.1	117	1	US-08-672-345C-13 Sequence 13, Appl
16	509	69.1	117	2	US-09-214-095D-13 Sequence 13, Appl
17	509	69.1	117	2	US-09-940-727B-13 Sequence 13, Appl
18	500.5	67.9	240	1	US-07-956-399-2 Sequence 2, Appl
19	500	67.8	121	1	US-08-887-352B-2 Sequence 2, Appl
20	500	67.8	121	2	US-09-109-207C-2 Sequence 2, Appl
21	500	67.8	121	2	US-09-296-005-2 Sequence 2, Appl
22	500	67.8	121	2	US-09-920-171-2 Sequence 2, Appl
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24	500	67.8	121	2	US-10-113-996-2 Sequence 2, Appl
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36	484	65.7	117	2	US-09-232-290-32 Sequence 32, Appl
37	482.5	65.5	241	2	US-08-902-486-13 Sequence 13, Appl
38	482.5	65.5	496	2	US-08-902-486-15 Sequence 15, Appl
39	473	64.2	117	1	US-08-672-345C-10 Sequence 10, Appl
40	473	64.2	117	1	US-08-672-345C-11 Sequence 11, Appl
41	473	64.2	117	1	US-08-672-345C-100 Sequence 100, App
42	473	64.2	117	1	US-08-672-345C-101 Sequence 101, App
43	473	64.2	117	2	US-09-214-095D-10 Sequence 10, Appl
44	473	64.2	117	2	US-09-214-095D-11 Sequence 11, Appl
45	473	64.2	117	2	US-09-940-727B-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1  
US-08-137-117D-31  
; Sequence 31, Application US/08137117D  
; Patent No. 5795965  
; GENERAL INFORMATION:  
; APPLICANT: TSUCHIYA, Masayuki  
; APPLICANT: SATO, Koh  
; APPLICANT: BENDIG, Mary  
; APPLICANT: JONES, Steven  
; APPLICANT: SALDANHA, Jose  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
; NUMBER OF SEQUENCES: 158  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/137,117D  
; FILING DATE: 20-DEC-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP92/00544  
; FILING DATE: 24-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-32084  
; FILING DATE: 19-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 3-95476  
; FILING DATE: 25-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 137 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-31

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Matches 114; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

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QY 121 TTYGYFDVWGQGTIVT 136
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RESULT 2
US-08-436-717-31
; Sequence 31, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-31

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Best Local Similarity 83.8%; Pred. No. 1.1e-49;
Matches 114; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLTCSVTGYSITSGYAWNWIQQFP 60
Db 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLTCTVTGYSITSDHAWSWIRQFP 60

QY 61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
Db 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120

QY 121 TTYGYFDVWGQGTIVT 136
Db 121 TT--AMDYWGQGTISVT 134

RESULT 3
US-08-767-128-18
; Sequence 18, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
```

```

; ; LENGTH: 119 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ; HYPOTHETICAL: NO
; ; ANTI-SENSE: NO
; ; FRAGMENT TYPE: internal
; ; ORIGINAL SOURCE:
; ;
US-08-767-128-18

Query Match 73.4%; Score 541; DB 2; Length 119;
Best Local Similarity 87.3%; Pred. No. 3.4e-45;
Matches 103; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

Qy 19 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIROFPGNKLEWMGYISYSGFTSY 78
Db 1 DVQLQESGPGLVKPSQSLTCTVTGYSTSDYAWNWIROFPGNKLEWMGYISYSGSTSY 60

Qy 79 NPSLRISFTRDTSKNQFFLQNLNSVTSEDATYYCARWDYGTYYGYFDVWGQTTVT 136
Db 61 NPSLKSIRISITRDTSKNQFFLQNLNSVTEDATYYCAR--CGNYPWFYDWGQTTLT 116

RESULT 4
US-08-308-494A-13
; Sequence 13, Application US/08308494A
; Patent No. 5959083
; GENERAL INFORMATION:
; APPLICANT: Bosslet, Klaus
; APPLICANT: Seeman, Gerhard
; TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
; TITLE OF INVENTION: Preparation and Use Thereof
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/308,494A
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,739
; FILING DATE: 01-JUN-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4118120.4
; FILING DATE: 03-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kulik, David J.
; REGISTRATION NUMBER: 36,576
; REFERENCE/DOCKET NUMBER: 05552-1186-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-308-494A-13
```

```

Query Match 71.3%; Score 525.5; DB 1; Length 117;
Best Local Similarity 85.2%; Pred. No. 1.1e-43;
Matches 98; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

Qy 22 LQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIROFPGNKLEWMGYISYSGFTSYNPS 81
Db 1 LQESGPDVLKPSQSLTCTVTGYSTSGYSHWIROFPGNKLEWMGYIQYSGITNYNPS 60

Qy 82 LRSRISFTRDTSKNQFFLQNLNSVTSEDATYYCARWDYGTYYGYFDVWGQTTVT 136
Db 61 LKSIRISITRDTSKNQFFLQNLNSVTEDATYYCAREDY-DYHWYFDVWGAGTTVT 114

RESULT 5
US-09-065-059-11
; Sequence 11, Application US/09065059
; Patent No. 6068841
; GENERAL INFORMATION:
; APPLICANT: SEINO, Ken-ichiro
; APPLICANT: KAYAGAKI, No. 6068841uhiko
; APPLICANT: YAGITA, Hideo
; APPLICANT: OKUMURA, KO
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,059
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: P-42,368
; REFERENCE/DOCKET NUMBER: 50356-151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-518-5100
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-065-059-11

Query Match 69.7%; Score 514; DB 2; Length 118;
Best Local Similarity 83.1%; Pred. No. 1.4e-42;
Matches 98; Conservative 8; Mismatches 8; Indels 4; Gaps 2;

Qy 20 VOLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIROFPGNKLEWMGYISYSGFTSYN 79
Db 1 VOLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIROFPGNKLEWMGYISYDGSNNYN 60

Qy 80 PSLRSRISFTRDTSKNQFFLQNLNSVTSEDATYYCARWDY-GTTYGYFDVWGQTTVT 136
Db 61 PSLKNRISITRDTSKNQFFLKLNSVTEDATYYCAVYYDGSS---FDYWGQTTVT 115

RESULT 6
US-08-913-555-11
```

```
; Sequence 11, Application US/08913555
; Patent No. 6946255
; GENERAL INFORMATION:
; APPLICANT: KAYAGAKI, No. 6946255uhiko
; APPLICANT: YAGITA, Kideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,555
; FILING DATE: 19-SEP-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: 42,368
; REFERENCE/DOCKET NUMBER: 50356-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-756-8600
; TELEFAX: 202-756-8699
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-913-555-11

Query Match 69.7%; Score 514; DB 2; Length 118;
Best Local Similarity 83.1%; Pred. No. 1.4e-42;
Matches 98; Conservative 8; Mismatches 8; Indels 4; Gaps 2;

QY 20 VQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIQFPGNKLEWMGYISYSGFTSYN 79
Db 1 VQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIQFPGNKLEWMGYISYDGSNNYN 60

QY 80 PSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWDY-GTTYGYFDVWGQGTTVT 136
Db 61 PSLKNRISITRDTSKNQFFLKLNSVTTEDATYYCAVYYDGS---FDYWGQGTTVT 115

RESULT 7
US-08-111-080-23
; Sequence 23, Application 08/111080
; Patent No. 5558865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-111-080-23

Query Match 69.3%; Score 510.5; DB 1; Length 114;
Best Local Similarity 83.1%; Pred. No. 3e-42;
Matches 98; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIQFPGNKLEWMGYISYSGFTSY 78
Db 1 EVQLQESGPGLVKPSQSLTCTVTGYSTITSDYAWNWIQFPGNKLEWMGYISYSGSTTY 60

QY 79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWDYGTYYGYFDVWGQGTTVT 136
Db 61 NPSLKSRISTRDTSKNLFLLQLSSVTSEDATYYCAR-----GSFGDWGQGTTLVT 111

RESULT 8
US-08-211-980-23
; Sequence 23, Application US/08211980
; Patent No. 5665569
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,980
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
```



```

;
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-980-23

Query Match 69.3%; Score 510.5; DB 1; Length 114;
Best Local Similarity 83.1%; Pred. No. 3e-42;
Matches 98; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIROPFGNKLWMMGYISYSGFTSY 78
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQESGPGLVKPSQSLTCTVTGYSTITSDYAWNWIROPFGNKLWMMGYISYSGSTTY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWDYGTYYGYFDVWGQGTTVT 136
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NPSLKSRSITRDTSKNLFQLSSVTSEDATYYCAR-----GSFGDWGQGTTLVT 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
PCT-US93-07967-23
; Sequence 23, Application PC/TUS9307967
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07967
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids

```

```

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-07967-23

Query Match 69.3%; Score 510.5; DB 5; Length 114;
Best Local Similarity 83.1%; Pred. No. 3e-42;
Matches 98; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIROPFGNKLWMMGYISYSGFTSY 78
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQESGPGLVKPSQSLTCTVTGYSTITSDYAWNWIROPFGNKLWMMGYISYSGSTTY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWDYGTYYGYFDVWGQGTTVT 136
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NPSLKSRSITRDTSKNLFQLSSVTSEDATYYCAR-----GSFGDWGQGTTLVT 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-08-466-151-7
; Sequence 7, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-7

Query Match 69.1%; Score 509.5; DB 2; Length 137;
Best Local Similarity 81.0%; Pred. No. 4.6e-42;

```

	Matches	98; Conservative	7; Mismatches	13; Indels	3; Gaps	1
Qy	19	DVQLQESGPGLVKPSQSLSLTCSVTGYSI	TSGYAWNWI	RQFPGNKLEWMGYI	SYSGFTSY	78
				:	:	
Db	1	DVQHQESEPDLVKPSQSLSLTCTVTGYSI	TSGYNRRHI	RQFPGNKLEWMGYI	IHYSGSTNY	60
				:	:	
Qy	79	NPSLRSRISFTTRDTSKNQFFLQLNSVTSE	DATYYCAR---	WDYGTTYGFVDWVGQGTTV		135
				:	:	
Db	61	NPSLKRRRISITRDTSKNQFFLQLNSVTTE	DATYYCARGS	IYYYGSRYRYFDWVGAGTTV		120
Qy	136	T	136			
Db	121	T	121			

```

RESULT 11
US-08-466-163B-7
; Sequence 7, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 7
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-466-163B-7

```

		Query Match	69.1%;	Score 509.5; DB 2;	Length 137;	
		Best Local Similarity	81.0%;	Pred. No. 4.6e-42;		
		Matches 98;	Conservative 7;	Mismatches 13;	Indels 3;	Gaps 1;
Qy	19	DVQLQESGPGLVKPSQSISLTCSVTGYSSITSGYAWNWIHQFPGNKLEWMGYIYSYGFTSY	78			
		:                                     :				
Db	1	DVQHQESEPDVLKPSQSISLTCVTGTGYSSITSGYNRHWIRQFPGNKLEWMGYIH YSGSTNY	60			
Qy	79	NPSLRSRISFTRDTSKNQOFFLQNSVTSSEDATYYCAR---	WDYGTTYGYFDVWGQTTV	135		
		:                                     :				
Db	61	NPSLKRRISITRDTSKNQOFFLQNSVTTEDATYYCARGSIYYGSRYRYFDVWGAGTIV	120			
Qy	136	T	136			
Db	121	T	121			

RESULT 12  
US-09-802-096-7  
; Sequence 7, Application US/09802096  
; Patent No. 6685939  
; GENERAL INFORMATION:  
; \*APPLICANT: Jardieu, Paula M.  
; \*APPLICANT: Presta, Leonard G.  
; \*TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
; \*FILE REFERENCE: P0718P2C3US  
; \*CURRENT APPLICATION NUMBER: US/09/802,096  
; \*CURRENT FILING DATE: 2001-03-08  
; \*PRIOR APPLICATION NUMBER: US 08/405,617  
; \*PRIOR FILING DATE: 1995-03-15  
; \*PRIOR APPLICATION NUMBER: US 08/185,899  
; \*PRIOR FILING DATE: 1994-01-26

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; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 7
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-802-096-7

```

	Query Match	69.1%;	Score 509.5;	DB 2;	Length 137;
	Best Local Similarity	81.0%;	Pred. No. 4.6e-42;		
	Matches 98;	Conservative 7;	Mismatches 13;	Indels 3;	Gaps 1
Qy	19 DVQLQESGPGLVKPSQSLSLTCSVTGYSIITSGYAWNWIRQPPGNKLEWMGYIISYSGFTSY	78			
Dd	1 DVQHQESEPDLVKPSQSLSLTCTVGTGSITSGYNRHWIRQPPGNKLEWMGYIHYSGSTNY	60			
Qy	79 NPSLRSRISFTRDTSKNQFFLQNSVTS EDTATYYCAR ---WDYGTTYGYFDVWGQTIV	135			
Dd	61 NP SLKRRISITRDTSKNQFFLQNSVTTEDTATYYCARGSIYYYGSRRYRYFDVWGAGTTV	120			
Qy	136 T 136				
Dd	121 T 121				

RESULT 13  
US-09-802-077-7  
; Sequence 7, Application US/09802077  
; Patent No. 6699472  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)  
; FILE REFERENCE: P0718P2C2US  
; CURRENT APPLICATION NUMBER: US/09/802,077  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: PCT/US92/06860  
; PRIOR FILING DATE: 1992-08-14  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 7  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-802-077-7

	Query Match	69.1%; Score 509.5; DB 2;	Length 137;
	Best Local Similarity	81.0%;	Pred. No. 4.6e-42;
	Matches	98; Conservative	7; Mismatches 13; Indels 3; Gaps 1
Qy	19 DVQLQESGPGLVKPSQSLSLTCSVTGYSIITSGYAWNWRQFPGNKLEWMGYIISYGFTSY	78	
Dd	1 DVHQESEPDLVKPSQSLSLTCTVGTYSITSGYNRHWIRQFPGNKLEWMGYIHYSGSTNY	60	
Qy	79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCAR -- WDYGTTYGFVDVWVGQTIV	135	
Dd	61 NPSLKRRISITRDTSKNQFFLQLNSVTTEDATYYCARGSIYYYGSRYRYFDVWGAGTIV	120	
Qy	136 T 136		
Dd	121 T 121		







GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:47:39 ; Search time 133.841 Seconds  
(without alignments)  
470.686 Million cell updates/sec

Title: US-09-889-936A-6  
Perfect score: 737  
Sequence: 1 MRVLILLWLFTAFPGILSDV.....WDYGTTRYGYFDVWGQTTVT 136

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	85.5	141	3	US-09-791-551-109
2	627.5	85.1	468	5	US-10-943-640-4
3	588	79.8	137	5	US-10-837-904-31
4	564.5	76.6	144	3	US-09-791-551-119
5	554	75.2	127	5	US-10-735-916A-52
6	554	75.2	127	6	US-11-012-353-52
7	544	73.8	121	4	US-10-310-674A-36
8	544	73.8	121	4	US-10-389-679-12
9	544	73.8	121	5	US-10-988-207-12
10	544	73.8	121	5	US-10-946-836A-12
11	539.5	73.2	730	6	US-11-035-599-30
12	539.5	73.2	730	6	US-11-035-599-31
13	539.5	73.2	761	6	US-11-035-599-29
14	539.5	73.2	762	6	US-11-035-599-28
15	535.5	72.7	140	3	US-09-874-141-53
16	532.5	72.3	115	4	US-10-308-817-131
17	532.5	72.3	115	4	US-10-453-698-131
18	527.5	71.6	118	5	US-10-735-916A-70
19	527.5	71.6	118	6	US-11-012-353-70
20	526	71.4	117	5	US-10-816-938-29
21	522	70.8	113	4	US-10-741-657A-19
22	518.5	70.4	118	4	US-10-184-300A-3
23	516	70.0	117	5	US-10-735-916A-69
24	516	70.0	117	6	US-11-012-353-69
25	512.5	69.5	136	3	US-09-858-349-2
26	512	69.5	113	4	US-10-741-657A-21
27	510	69.2	265	4	US-10-689-006-22

28	509.5	69.1	137	3	US-09-802-077-7	Sequence 7, Appli
29	509.5	69.1	137	3	US-09-802-096-7	Sequence 7, Appli
30	509.5	69.1	137	3	US-09-925-179-7	Sequence 7, Appli
31	509.5	69.1	137	5	US-10-968-237-7	Sequence 7, Appli
32	509	69.1	117	3	US-09-940-727B-13	Sequence 13, Appl
33	509	69.1	119	4	US-10-713-248-3	Sequence 3, Appli
34	509	69.1	119	4	US-10-713-248-7	Sequence 7, Appli
35	508.5	69.0	118	5	US-10-735-916A-71	Sequence 71, Appl
36	508.5	69.0	118	6	US-11-012-353-71	Sequence 71, Appl
37	502.5	68.2	118	4	US-10-372-481-17	Sequence 17, Appl
38	502.5	68.2	118	4	US-10-371-797-17	Sequence 17, Appl
39	501	68.0	135	5	US-10-735-916A-77	Sequence 77, Appl
40	501	68.0	135	6	US-11-012-353-77	Sequence 77, Appl
41	500	67.8	121	3	US-09-920-171-2	Sequence 2, Appli
42	500	67.8	121	4	US-10-113-996-2	Sequence 2, Appli
43	500	67.8	121	5	US-10-791-619-2	Sequence 2, Appli
44	500	67.8	130	3	US-09-802-077-5	Sequence 5, Appli
45	500	67.8	130	3	US-09-802-096-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-09-791-551-109  
; Sequence 109, Application US/09791551  
; Publication No. US20030235584A1  
; GENERAL INFORMATION:  
; APPLICANT: KLOETZER, WILLIAM S.  
; APPLICANT: HANNA, NABIL  
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES  
; FILE REFERENCE: 037003/0277869  
; CURRENT APPLICATION NUMBER: US/09/791,551  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/185,390  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/233,625  
; PRIOR FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 119  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 109  
; LENGTH: 141  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-791-551-109

Query Match	85.5%	Score	630;	DB	3;	Length	141;
Best Local Similarity	86.8%	Pred. No.	2e-49;				
Matches	118;	Conservative	6;	Mismatches	12;	Indels	0;
						Gaps	0;
Qy	1	MRVLILLWLFTAFPGILSDVQLQESGGLVKPSQSLTCSVTGYSTITSGYAMNWIQFP	60				
Db	1	MRVLILLWLFTAFPGILSDVQLQESGGLVKPSQSLTCTVTGSSITSDYAWHWIRQFP	60				
Qy	61	GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLSNVTSEDATYYICARWDYG	120				
Db	61	GNKLEWMGYISFSGSTGYNPSLKSFRFSITRDTSKNQFFLQLSNVTTEDATYYICAREAYG	120				
Qy	121	TTYGYFDVWGQTTVT	136				
Db	121	YDVGYFDYWGQTTLT	136				

RESULT 2  
US-10-943-640-4  
; Sequence 4, Application US/10943640  
; Publication No. US20050152907A1  
; GENERAL INFORMATION:  
; APPLICANT: LIANG, Tony W.  
; APPLICANT: LOO, Deryk T.  
; APPLICANT: XU, Xiaolin  
; TITLE OF INVENTION: KID3 AND KID3 ANTIBODIES THAT BIND  
; TITLE OF INVENTION: THERETO

FILE REFERENCE: 415072002700  
CURRENT APPLICATION NUMBER: US/10/943,640  
CURRENT FILING DATE: 2004-09-17  
PRIOR APPLICATION NUMBER: US 60/504,441  
PRIOR FILING DATE: 2003-09-18  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 468  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Construct  
US-10-943-640-4  
  
Query Match 85.1%; Score 627.5; DB 5; Length 468;  
Best Local Similarity 87.5%; Pred. No. 1.2e-48;  
Matches 119; Conservative 6; Mismatches 10; Indels 1; Gaps 1;  
  
QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIROFP 60  
Db 1 MGVLLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIROFP 60  
  
QY 61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYICARWDYG 120  
Db 61 GNKLEWMGYISYSGFTSYNPSLRSRISITRDTSKNQFFLQLNSVTTEDATYICARFYR 120  
  
QY 121 TTYGYFDVWGQGTTVT 136  
Db 121 YA-DYFDYWGQGTTLT 135

RESULT 3  
US-10-837-904-31  
Sequence 31, Application US/10837904  
Publication No. US20050142635A1  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
SATO, Koh  
JONES, Mary Margaret  
JONES, Steven Tarran  
SALDANHA, Jose William  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
INTERLEUKIN-6 RECEPTOR  
NUMBER OF SEQUENCES: 134  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/837,904  
FILING DATE: 04-May-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/114,285  
FILING DATE: 13-Jul-1998  
APPLICATION NUMBER: US 08/436,717  
FILING DATE: 08-MAY-1995  
APPLICATION NUMBER: US 08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
APPLICATION NUMBER: JP 3-95476

FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Wegner, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/234  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-10-837-904-31  
  
Query Match 79.8%; Score 588; DB 5; Length 137;  
Best Local Similarity 83.8%; Pred. No. 1.2e-45;  
Matches 114; Conservative 8; Mismatches 12; Indels 2; Gaps 1;  
  
QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIROFP 60  
Db 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCTVTGYSITSDHAWSWIROFP 60  
  
QY 61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYICARWDYG 120  
Db 61 GNKLEWMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYICARSLAR 120  
  
QY 121 TTYGYFDVWGQGTTVT 136  
Db 121 TT--AMDYWGQGTSTV 134

RESULT 4  
US-09-791-551-119  
Sequence 119, Application US/09791551  
Publication No. US20030235584A1  
GENERAL INFORMATION:  
APPLICANT: KLOETZER, WILLIAM S.  
HANNA, NABIL  
TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES  
FILE REFERENCE: 037003/0277869  
CURRENT APPLICATION NUMBER: US/09/791,551  
CURRENT FILING DATE: 2001-02-26  
PRIOR APPLICATION NUMBER: 60/185,390  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: 60/233,625  
PRIOR FILING DATE: 2000-09-18  
NUMBER OF SEQ ID NOS: 119  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 119  
LENGTH: 144  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-791-551-119

Query Match 76.6%; Score 564.5; DB 3; Length 144;  
Best Local Similarity 78.4%; Pred. No. 1.8e-43;  
Matches 109; Conservative 9; Mismatches 18; Indels 3; Gaps 1;  
  
QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIROFP 60  
Db 1 MMVLSLLYLLTAIPGILSDVQLQESGPGDLVKPSQSLSLTCSVTGYSITSGYAWNWIROFP 60  
  
QY 61 GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYICARWD-- 118  
Db 61 GNKLEWVGYLSYDGSKSHNPSLRNRISITRDPKSNQFFLKLNSVTTEDATYICARGGKI 120  
  
QY 119 -YGTTYGYFDVWGQGTTVT 136  
Db 121 FYGSSYDPFAYWGQGTTLV 139









		Matches	104;	Conservative	12;	Mismatches	19;	Indels	1;	Gaps	1;
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Db	1	MMVLSLLYLLTALPGFLSEVQLQESGPSLVKPSQTL	SLTCSVTGDSITNGF	-W	I	WIR	KEP	59			
Qy	61	GNKLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQ	NSVTSED	TATYY	CAR	WDY	120				
Db	60	GNKLEYMGYISYSGSTYYNPSLKSRI	SITRDTSONQFYLQ	NSVT	TEDT	G	119				
Qy	121	TTYGYFDVWGQGT	TVT	136							
Db	120	RTPYFD	FWGQGT	TLT	135						

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Job time : 134.841 secs

GenCore version 5.1.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 17:49:02 ; Search time 6.47619 Seconds  
(without alignments)  
44.858 Million cell updates/sec

Title: US-09-889-936A-6  
Perfect score: 737  
Sequence: 1 MRVLLLLWLFAPPGILSDV.....WDYGTYYGYFDVWGQGTTVT 136

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	491	66.6	117	7	US-11-219-121-11 Sequence 11, Appl
2	491	66.6	146	7	US-11-219-121-13 Sequence 13, Appl
3	429	58.2	466	7	US-11-211-917-30 Sequence 30, Appl
4	429	58.2	466	7	US-11-211-917-70 Sequence 70, Appl
5	424	57.5	466	7	US-11-211-917-86 Sequence 86, Appl
6	419.5	56.9	118	7	US-11-211-917-142 Sequence 142, App
7	419	56.9	118	6	US-10-981-300-51 Sequence 51, Appl
8	418	56.7	118	6	US-10-981-300-54 Sequence 54, Appl
9	418	56.7	443	6	US-10-981-300-20 Sequence 20, Appl
10	417.5	56.6	118	7	US-11-211-917-109 Sequence 109, App
11	412	55.9	121	7	US-11-211-917-26 Sequence 26, Appl
12	412	55.9	121	7	US-11-211-917-98 Sequence 98, Appl
13	410	55.6	121	7	US-11-211-917-66 Sequence 66, Appl
14	409.5	55.6	115	6	US-10-981-300-53 Sequence 53, Appl
15	407	55.2	121	7	US-11-211-917-82 Sequence 82, Appl
16	399	54.1	451	7	US-11-254-182-43 Sequence 43, Appl
17	398	54.0	451	7	US-11-254-182-41 Sequence 41, Appl
18	398	54.0	451	7	US-11-254-182-42 Sequence 42, Appl
19	396	53.7	286	7	US-11-154-103-8 Sequence 8, Appl
20	396	53.7	464	7	US-11-211-917-22 Sequence 22, Appl
21	393	53.3	118	6	US-10-981-300-52 Sequence 52, Appl
22	393	53.3	180	6	US-10-981-300-4 Sequence 4, Appl
23	390	52.9	447	7	US-11-219-121-32 Sequence 32, Appl
24	386.5	52.4	120	7	US-11-211-917-108 Sequence 108, App
25	379	51.4	119	7	US-11-211-917-18 Sequence 18, Appl

26	376	51.0	117	7	US-11-219-121-26	Sequence 26, Appl
27	376	51.0	447	7	US-11-219-121-30	Sequence 30, Appl
28	373.5	50.7	118	6	US-10-983-104-8	Sequence 8, Appl
29	351	47.6	121	7	US-11-219-563-84	Sequence 84, Appl
30	351	47.6	121	7	US-11-219-563-89	Sequence 89, Appl
31	351	47.6	121	7	US-11-219-563-90	Sequence 90, Appl
32	342.5	46.5	471	7	US-11-106-762-25	Sequence 25, Appl
33	342.5	46.5	471	7	US-11-106-762-27	Sequence 27, Appl
34	340.5	46.2	120	7	US-11-254-679-15	Sequence 15, Appl
35	336	45.6	123	7	US-11-254-182-36	Sequence 36, Appl
36	335	45.5	123	7	US-11-254-182-34	Sequence 34, Appl
37	329	44.6	123	7	US-11-211-917-117	Sequence 117, App
38	327.5	44.4	120	7	US-11-230-593A-31	Sequence 31, Appl
39	325.5	44.2	291	7	US-11-154-103-10	Sequence 10, Appl
40	325	44.1	123	7	US-11-211-917-116	Sequence 116, App
41	325	44.1	470	7	US-11-211-917-78	Sequence 78, Appl
42	324	44.0	123	7	US-11-211-917-115	Sequence 115, App
43	322.5	43.8	452	7	US-11-106-762-34	Sequence 34, Appl
44	322.5	43.8	452	7	US-11-106-762-36	Sequence 36, Appl
45	321.5	43.6	120	7	US-11-230-593A-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1  
US-11-219-121-11  
; Sequence 11, Application US/11219121  
; Publication No. US20060093601A1  
; GENERAL INFORMATION:  
; APPLICANT: Fong, Sherman  
; APPLICANT: Dennis Mark S.  
; TITLE OF INVENTION: HUMANIZED ANTI-BETA7 ANTAGONISTS AND USES THEREFOR  
; FILE REFERENCE: P2159R1  
; CURRENT APPLICATION NUMBER: US/11/219,121  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 60/607,377  
; PRIOR FILING DATE: 2004-09-03  
; NUMBER OF SEQ ID NOS: 68  
; SEQ ID NO 11  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: sequence is synthesized  
US-11-219-121-11

Query Match 66.6%; Score 491; DB 7; Length 117;  
Best Local Similarity 79.7%; Pred. No. 6.7e-31;  
Matches 94; Conservative 8; Mismatches 12; Indels 4; Gaps 2;  
Qy 19 DVQLQESGPGLVKPSQSLTCSVTGYTSITSGYAWNWIROPFGNKLWGMGYISYSGFTSY 78  
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Db 1 EVQLQESGPGLVKPSQSLTCSVTGFFITNNY-WGWIRKPPGNKMEWMGYISYSGSTSY 59  
Qy 79 NPSLRSRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGYFDVWGQGTTVT 136  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 60 NPSLKSRISTRDTSKNQFFLQNSVTEDATYYCAMTG---SSGYFDWGPPTMTVT 114

RESULT 2  
US-11-219-121-13  
; Sequence 13, Application US/11219121  
; Publication No. US20060093601A1  
; GENERAL INFORMATION:  
; APPLICANT: Fong, Sherman  
; APPLICANT: Dennis Mark S.  
; TITLE OF INVENTION: HUMANIZED ANTI-BETA7 ANTAGONISTS AND USES THEREFOR  
; FILE REFERENCE: P2159R1  
; CURRENT APPLICATION NUMBER: US/11/219,121  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 60/607,377  
; PRIOR FILING DATE: 2004-09-03

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; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 13
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-219-121-13

Query Match          66.6%; Score 491; DB 7; Length 146;
Best Local Similarity 79.7%; Pred. No. 8.1e-31;
Matches 94; Conservative 8; Mismatches 12; Indels 4; Gaps 2;

QY 19 DVQLQESGGLVKPQSLSLTCSVTGYISITSGYAWNWIROFPGNKLEWMGYISYSGFTSY 78
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLQESGGLVKPQSLSLTCSVTGFFITNNY-WGWIRKFPFGNKMWMGYISYSGSTSY 59

QY 79 NPSLRSRISFTRDTSKNQFFLQNSVTSEDATYYICARWDYGTYYGYFDVWGQGTVT 136
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 NPSLKSRISTRDTSKNQFFLQNSVTTEDATYYICAMTG---SSGYFDVWGPGTMT 114

RESULT 3
US-11-211-917-30
; Sequence 30, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-30

Query Match          58.2%; Score 429; DB 7; Length 466;
Best Local Similarity 64.4%; Pred. No. 8.5e-26;
Matches 87; Conservative 15; Mismatches 27; Indels 6; Gaps 4;

QY 7 LWLF---TAFP-GILSDVQLQESGGLVKPQSLSLTCSVTGYISITSGYAWNWIROFPGN 62
; ||| | | | : || | || | || | || | || | : || | || | || | || |
Db 4 LWFFLLLVAAAPRWLSQVQLQESGGLVKPSETLSLTCTVSGGSI-RGYVSWIRQPPGK 62

QY 63 KLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQNSVTSEDATYYICARWD--YG 120
; |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 GLEWIGYIYSGSTNYNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARKGGLYG 122

QY 121 TTYGYFDVWGQGTVT 136
; |||: || | || | || | || |
Db 123 -DYGWFAFWGQGTTLVT 137

RESULT 5
US-11-211-917-86
; Sequence 86, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR FILING DATE: 2005-08-25
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-86

Query Match          57.5%; Score 424; DB 7; Length 466;
Best Local Similarity 64.7%; Pred. No. 2e-25;
Matches 88; Conservative 16; Mismatches 24; Indels 8; Gaps 5;

QY 7 LWLF---TAFP-GILSDVQLQESGGLVKPQSLSLTCSVTGYISITSGYAWNWIROFPGN 62
; ||| | | | : || | || | || | || | || | : || | || | || | || |
Db 4 LWFFLLLVAAAPRWLSQVQLQESGGLVKPSETLSLTCTVSGGSI-RGYVSWIRQPPGK 62

QY 63 KLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQNSVTSEDATYYICARWD--YG 120
; |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 GLEWIGYIYSGSTNYNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARRGGLYG 122
```

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; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-70

Query Match          58.2%; Score 429; DB 7; Length 466;
Best Local Similarity 65.4%; Pred. No. 8.5e-26;
Matches 89; Conservative 15; Mismatches 24; Indels 8; Gaps 5;

QY 7 LWLF---TAFP-GILSDVQLQESGGLVKPQSLSLTCSVTGYISITSGYAWNWIROFPGN 62
; ||| | | | : || | || | || | || | || | : || | || | || | || |
Db 4 LWFFLLLVAAAPRWLSQVQLQESGGLVKPSETLSLTCTVSGGSI-RGYVSWIRQPPGK 62

QY 63 KLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQNSVTSEDATYYICARWD--YG 120
; |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 GLEWIGYIYSGSTNYNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARKGGLYG 122

QY 121 TTYGYFDVWGQGTVT 136
; |||: || | || | || | || |
Db 123 -DYGWFAFWGQGTTLVT 137

RESULT 5
US-11-211-917-86
; Sequence 86, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-86

Query Match          57.5%; Score 424; DB 7; Length 466;
Best Local Similarity 64.7%; Pred. No. 2e-25;
Matches 88; Conservative 16; Mismatches 24; Indels 8; Gaps 5;

QY 7 LWLF---TAFP-GILSDVQLQESGGLVKPQSLSLTCSVTGYISITSGYAWNWIROFPGN 62
; ||| | | | : || | || | || | || | || | : || | || | || | || |
Db 4 LWFFLLLVAAAPRWLSQVQLQESGGLVKPSETLSLTCTVSGGSI-RGYVSWIRQPPGK 62

QY 63 KLEWMGYISYSGFTSYNPSLRSRISFTRDTSKNQFFLQNSVTSEDATYYICARWD--YG 120
; |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 GLEWIGYIYSGSTNYNPSLKSRTVISVDTSKNQFSLKLSVTAADTAVYYCARRGGLYG 122
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Qy 121 TTYGYFDVWGQGTTVT 136  
Db 123 -DYGWEAPWGQGTTLVT 137

RESULT 6  
US-11-211-917-142  
; Sequence 142, Application US/112111917  
; Publication No. US20060093600A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/11/211,917  
; CURRENT FILING DATE: 2005-08-25  
; PRIOR APPLICATION NUMBER: US/10/292,088  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 142  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-211-917-142

Query Match 56.9%; Score 419.5; DB 7; Length 118;  
Best Local Similarity 70.1%; Pred. No. 1.3e-25;  
Matches 82; Conservative 16; Mismatches 16; Indels 3; Gaps 3;  
Qy 20 VQLQESGPGLVKPSQSLTCSVTGYSTITSGYANNWIRQPPGNKLEWMGYISYSGFTSYN 79  
Db 2 VQLQESGPGLVKPSQSLTCTVSGSIS-YYWSWIRQPPGKLEWIGIYIYSGSTNYN 60  
Qy 80 PSLSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136  
Db 61 PSLSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-DYG-DYNWFDPWGQGTTLVT 115

RESULT 7  
US-10-981-300-51  
; Sequence 51, Application US/10981300  
; Publication No. US20060093599A1  
; GENERAL INFORMATION:  
; APPLICANT: GIORGIO SENALDI  
; APPLICANT: GADI GAZIT-BORNSTEIN  
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS  
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME  
; FILE REFERENCE: ABGX-005  
; CURRENT APPLICATION NUMBER: US/10/981,300  
; CURRENT FILING DATE: 2004-11-03  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 51  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-981-300-51

Query Match 56.9%; Score 419; DB 6; Length 118;  
Best Local Similarity 69.5%; Pred. No. 1.4e-25;  
Matches 82; Conservative 13; Mismatches 17; Indels 6; Gaps 2;  
Qy 20 VQLQESGPGLVKPSQSLTCSVTGYSTITSGYANNWIRQPPGNKLEWMGYISYSGFTSY 78  
Db 2 VQLQESGPGLVKPSQTLTSLTCTVSGSISGGYYWSWIRQHPGKLEWIGIYIYSGSTYY 61  
Qy 79 NPSLSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136

Db 62 NPSLSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-----TGDFYDWGQGTTLVT 114  
RESULT 8  
US-10-981-300-54  
; Sequence 54, Application US/10981300  
; Publication No. US20060093599A1  
; GENERAL INFORMATION:  
; APPLICANT: GIORGIO SENALDI  
; APPLICANT: GADI GAZIT-BORNSTEIN  
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS  
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME  
; FILE REFERENCE: ABGX-005  
; CURRENT APPLICATION NUMBER: US/10/981,300  
; CURRENT FILING DATE: 2004-11-03  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 54  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-981-300-54

Query Match 56.7%; Score 418; DB 6; Length 118;  
Best Local Similarity 68.4%; Pred. No. 1.6e-25;  
Matches 80; Conservative 16; Mismatches 17; Indels 4; Gaps 2;  
Qy 20 VQLQESGPGLVKPSQSLTCSVTGYSTITSGYANNWIRQPPGNKLEWMGYISYSGFTSYN 79  
Db 2 VQLQESGPGLVKPSQSLTCTVSGGSI-SIYYWSWIRQPPGKLEWIGIYIYSGSTNYN 60  
Qy 80 PSLSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136  
Db 61 PSLSRVTISVDTSKNQFSLKLSVTAADTAVYYCAVWNYGDA---FDIWGQGTMTV 114

RESULT 9  
US-10-981-300-20  
; Sequence 20, Application US/10981300  
; Publication No. US20060093599A1  
; GENERAL INFORMATION:  
; APPLICANT: GIORGIO SENALDI  
; APPLICANT: GADI GAZIT-BORNSTEIN  
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS  
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME  
; FILE REFERENCE: ABGX-005  
; CURRENT APPLICATION NUMBER: US/10/981,300  
; CURRENT FILING DATE: 2004-11-03  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 443  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-10-981-300-20

Query Match 56.7%; Score 418; DB 6; Length 443;  
Best Local Similarity 68.4%; Pred. No. 5.3e-25;  
Matches 80; Conservative 16; Mismatches 17; Indels 4; Gaps 2;  
Qy 20 VQLQESGPGLVKPSQSLTCSVTGYSTITSGYANNWIRQPPGNKLEWMGYISYSGFTSYN 79  
Db 2 VQLQESGPGLVKPSQSLTCTVSGGSI-SIYYWSWIRQPPGKLEWIGIYIYSGSTNYN 60  
Qy 80 PSLSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTTYGYFDVWGQGTTVT 136  
Db 61 PSLSRVTISVDTSKNQFSLKLSVTAADTAVYYCAVWNYGDA---FDIWGQGTMTV 114

RESULT 10  
US-11-211-917-109  
; Sequence 109, Application US/112111917

```

; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-109

Query Match      56.6%; Score 417.5; DB 7; Length 118;
Best Local Similarity 70.1%; Pred. No. 1.8e-25;
Matches 82; Conservative 15; Mismatches 17; Indels 3; Gaps 3;

Qy      20 VQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIROPFGNKLEWMGYISYSGFTSYN 79
Db      2 VQLQESGPGLVKPSSETLSLTCTVSGGSISS-YYWSWIRQPPGKGLEWIGIYYSGSTNYN 60

Qy      80 PSLRSRISFTRDTSKNQFFLQNSVTSEDATATYYCARWDYGTYYGYFDVWGQGTTVT 136
Db      61 PSLKSRVTISVDTSKNQFSLKLSSTAAADTAVYYCAR-DYGGN-SYFDYWGQGTTLVT 115

RESULT 11
US-11-211-917-26
; Sequence 26, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-26

Query Match      55.9%; Score 412; DB 7; Length 121;
Best Local Similarity 67.8%; Pred. No. 4.6e-25;
Matches 80; Conservative 14; Mismatches 22; Indels 2; Gaps 2;

Qy      20 VQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIROPFGNKLEWMGYISYSGFTSYN 79
Db      2 VQLQESGPGLVKPSSETLSLTCTVSGGSISS-YYWTWIRQPPGKGLEWIGIYYSGSTNYN 60

Qy      80 PSLRSRISFTRDTSKNQFFLQNSVTSEDATATYYCAR-WDYGTYYGYFDVWGQGTTVT 136
Db      61 PSLKSRVTISVDMSKNQFSLKLSSTAAADTAVYYCAR-KGDYGGNFNFHWGQGTTLVT 118

RESULT 12
US-11-211-917-98
; Sequence 98, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-98

Query Match      55.9%; Score 412; DB 7; Length 121;
Best Local Similarity 68.9%; Pred. No. 4.6e-25;
Matches 82; Conservative 14; Mismatches 19; Indels 4; Gaps 3;

Qy      20 VQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIROPFGNKLEWMGYISYSGFTSYN 79
Db      2 VQLQESGPGLVKPSSETLSLTCTVSGGSI-RCYYWSWIRQPPGKGLEWIGIYYSGSTNYN 60

Qy      80 PSLRSRISFTRDTSKNQFFLQNSVTSEDATATYYCARWD--YGTYYGYFDVWGQGTTVT 136
Db      61 PSLKSRVTISVDTSKNQFSLKLSVTAAADTAVYYCAR-KGGLYG-DYGFAPWGQGTTLVT 118

RESULT 13
US-11-211-917-66
; Sequence 66, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-66

Query Match      55.6%; Score 410; DB 7; Length 121;
Best Local Similarity 68.9%; Pred. No. 6.5e-25;
Matches 82; Conservative 13; Mismatches 20; Indels 4; Gaps 3;

Qy      20 VQLQESGPGLVKPSQSLTCSVTGYSTITSGYAWNWIROPFGNKLEWMGYISYSGFTSYN 79
Db      2 VQLQESGPGLVKPSSETLSLTCTVSGGSISS-YYWTWIRQPPGKGLEWIGIYYSGSTNYN 60
```

Db 2 VQLQESGPGLVKPSDTLSLTCTVSGGSI-RGYYSWIRQPPGKGLEWIGYIYSGSTNYN 60  
Qy 80 PSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWD--YGTTYGYFDVWVGQTTVT 136  
Db 61 PSLKSRVTISVDTSKNQFSLKLNSTAAATAVYYCARKGGLYG-DYGFAPWGQGTILVT 118

RESULT 14  
US-10-981-300-53  
; Sequence 53, Application US/10981300  
; Publication No. US20060093599A1  
; GENERAL INFORMATION:  
; APPLICANT: GIORGIO SENALDI  
; APPLICANT: GADI GAZIT-BORNSTEIN  
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS  
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME  
; FILE REFERENCE: ABGX-005  
; CURRENT APPLICATION NUMBER: US/10/981,300  
; CURRENT FILING DATE: 2004-11-03  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-981-300-53

Query Match 55.6%; Score 409.5; DB 6; Length 115;  
Best Local Similarity 67.5%; Pred. No. 6.7e-25;  
Matches 79; Conservative 17; Mismatches 14; Indels 7; Gaps 3;  
Qy 20 VQLQESGPGLVKPSQSLTCSVTGYISITSGYAWNIRQPPGNKLEWMGYISYSGFTSYN 79  
Db 2 VQLQESGPGLVKPSSETLSLTCTVSGGSISS-YYWSWIRQPPGKGLEWIGYIYSGSTNYN 60  
Qy 80 PSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWDYGTTTYGYFDVWVGQTTVT 136  
Db 61 PSLKSRVTISVDTSKNQFSLKLNSTAAATAVYYCA-WNYA-----FDIWGQGTMT 111

RESULT 15  
US-11-211-917-82  
; Sequence 82, Application US/11211917  
; Publication No. US20060093600A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/11/211,917  
; CURRENT FILING DATE: 2005-08-25  
; PRIOR APPLICATION NUMBER: US/10/292,088  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-211-917-82

Query Match 55.2%; Score 407; DB 7; Length 121;  
Best Local Similarity 68.1%; Pred. No. 1.1e-24;  
Matches 81; Conservative 15; Mismatches 19; Indels 4; Gaps 3;  
Qy 20 VQLQESGPGLVKPSQSLTCSVTGYISITSGYAWNIRQPPGNKLEWMGYISYSGFTSYN 79  
Db 2 VQLQESGPGLVKPSSETLSLTCTVSGGSI-RGYYSWIRQPPGKGLEWIGYIYSGSTNYN 60

Qy 80 PSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCARWD--YGTTYGYFDVWVGQTTVT 136  
Db 61 PSLKSRVTISVDTSKNQFSLKLNSTAAATAVYYCARRGGLYG-DYGFAPWGQGTILVT 118  
Search completed: May 19, 2006, 17:53:13  
Job time : 7.47619 secs





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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:34:57 ; Search time 135.333 Seconds  
(without alignments)  
391.900 Million cell updates/sec

Title: US-09-889-936A-8  
Perfect score: 606  
Sequence: 1 SRGDIVMTQSPSSLVSAGE.....QNDHIYPYTFGGGTKLEIK 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A Geneseq\_8:\*
- 1: geneseqp1980s:\*
  - 2: geneseqp1990s:\*
  - 3: geneseqp2000s:\*
  - 4: geneseqp2001s:\*
  - 5: geneseqp2002s:\*
  - 6: geneseqp2003as:\*
  - 7: geneseqp2003bs:\*
  - 8: geneseqp2004s:\*
  - 9: geneseqp2005s:\*
  - 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	606	100.0	116	3 AAB15673	Aab15673 Murine 5B
2	545	89.9	113	7 ADD94117	Add94117 Mouse HUI
3	545	89.9	113	9 ADV66167	Adv66167 Human EpC
4	545	89.9	113	9 ADZ83525	Adz83525 AntiEpCam
5	545	89.9	248	2 AAY17960	Aay17960 Mouse scF
6	545	89.9	497	9 ADZ83445	Adz83445 CD3 speci
7	545	89.9	500	9 ADV66137	Adv66137 Anti-CD3-
8	545	89.9	503	9 ADV66133	Adv66133 Anti-CD3-
9	545	89.9	503	9 ADV66135	Adv66135 Anti-CD3-
10	545	89.9	515	9 ADZ83436	Adz83436 Deimmuniz
11	545	89.9	521	9 ADV66116	Adv66116 Anti-CD3-
12	540	89.1	114	4 AAB62864	Aab62864 Anti-SAF-
13	536	88.4	113	2 AAR38603	Aar38603 MCPC ligh
14	536	88.4	113	2 AAR68742	Aar68742 MAB MCP6
15	536	88.4	113	2 AAW58483	Aaw58483 Murine MC
16	536	88.4	113	8 ADI01145	Adi01145 Murine MC
17	536	88.4	115	2 AAR52036	Aar52036 Light cha
18	536	88.4	115	8 ADO32152	Ado32152 Mouse ant
19	536	88.4	118	9 AED64796	Aed64796 Murine an
20	536	88.4	220	2 AAR53802	Aar53802 FAB light
21	535	88.3	113	2 AAW42468	Aaw42468 Fab15 lig
22	534	88.1	116	1 AAP80460	Aap80460 Sequence
23	534	88.1	277	2 AAR39336	Aar39336 scFv frag

24	532	87.8	113	2 AAR54102	Aar54102 Humanised
25	532	87.8	113	2 AAW42467	Aaw42467 Fab2 ligh
26	528	87.1	113	2 AAR90834	Aar90834 17F6 ligh
27	526	86.8	113	2 AAR98479	Aar98479 MAB 2B6 1
28	526	86.8	113	2 AAW42452	Aaw42452 Mouse ant
29	526	86.8	679	10 AEF80923	Aef80923 Staphyloc
30	525	86.6	482	2 AAY06915	Aay06915 Amino aci
31	523	86.3	118	7 ADD13796	Add13796 Plasmid p
32	521	86.0	113	2 AAR90839	Aar90839 14G1 ligh
33	520	85.8	263	7 ADG32320	Adg32320 Mouse scF
34	518	85.5	115	3 AAB28395	Aab28395 Anti-VEGF
35	518	85.5	115	5 AAU77947	Aau77947 Variable
36	516	85.1	113	6 ABO10744	Abol0744 Variable
37	516	85.1	113	6 ABO10756	Abol0756 Variable
38	516	85.1	113	6 ABR44700	Abr44700 Murine Mu
39	516	85.1	113	6 ABR44688	Abr44688 Murine Mu
40	516	85.1	113	8 ADQ90822	Adq90822 Kabat sub
41	516	85.1	113	8 ADU67950	Adu67950 Mouse Kab
42	516	85.1	113	8 ADU67970	Adu67970 Mouse Kab
43	516	85.1	113	9 AED41851	Aed41851 Mouse pro
44	516	85.1	113	9 AED41871	Aed41871 Mouse pro
45	513	84.7	113	9 ADV66175	Adv66175 Human EpC

ALIGNMENTS

RESULT 1  
AAB15673  
ID AAB15673 standard; protein; 116 AA.  
XX  
AC AAB15673;  
XX  
DT 08-JAN-2001 (first entry)  
XX  
DE Murine 5B3 antibody light chain variable region.  
XX  
KW Mouse; 5B3 antibody; IgG1; piezoelectric immunoassay;  
KW small molecule explosive detection; 2,4,6-trinitrotoluene; TNT.  
XX  
OS Mus sp.  
XX  
PN WO200043774-A2.  
XX  
PD 27-JUL-2000.  
XX  
PF 25-JAN-2000; 2000WO-IL0000048.  
XX  
PR 25-JAN-1999; 99IL-00128212.  
XX  
(YISS ) YISSUM RES & DEV CO.  
(YEDA ) YEDA RES & DEV CO LTD.  
PI Willner I, Eshhar Z;  
XX  
DR WPI; 2000-524259/47.  
DR N-PSDB; AAA74605.  
XX  
PT Apparatus for detecting small molecules, especially explosives comprises  
PT a piezoelectric crystal.  
XX  
PS Disclosure; Fig 3B; 90pp; English.  
XX  
CC The present sequence is the light chain variable region of 5B3 antibody.  
CC The cDNA encoding this sequence was obtained from total RNA extracted  
CC from a 5B3 hybridoma by RT-PCR. 5B3 is an IgG1 antibody derived from a  
CC TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked  
CC by very low amounts of TNT and it can therefore be used in a method for  
CC detecting small assayed explosive molecules. Molecules are detected using  
CC a piezoelectric sensor. Piezoelectric immunoassaying in liquid phase  
CC allows stationary and flow analysis of an aqueous sample. The method is  
CC sufficiently sensitive for detection of low molecular weight molecules

SQ Sequence 116 AA;
Query Match 100.0%; Score 606; DB 3; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRGDIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYG 60
Db 1 SRGDIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYG 60

QY 61 FIRDSGVPDRFTGSGSGTDFTLTISSSVQAEDLAVYYCQNDHIYPTTFGGGTKLEIK 116
Db 61 FIRDSGVPDRFTGSGSGTDFTLTISSSVQAEDLAVYYCQNDHIYPTTFGGGTKLEIK 116

RESULT 2
ADD94117
ID ADD94117 standard; protein; 113 AA.
XX
AC ADD94117;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse HUIV26 variable region light chain partial amino acid sequence.
XX
KW grafted antibody; complementarity determining region; CDR; light CDR;
KW heavy CDR; cryptic collagen epitope; solid tumour;
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW collagen agonist; collagen antagonist; cancer metastasis;
KW anti-cryptic collagen; antibody; HUIV26; variable region light chain;
KW mouse; murine.
XX
OS Mus musculus.
XX
PN WO2003046204-A2.
XX
PD 05-JUN-2003.
XX
PF 26-NOV-2002; 2002WO-US038147.
XX
PR 26-NOV-2001; 2001US-00995529.
PR 06-DEC-2001; 2001US-00011250.
XX
PA (CELL-) CELL MATRIX INC.
XX
PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX
DR WPI; 2003-513649/48.
DR N-PSDB; ADD94116.
XX
PT New cryptic collagen antibody with one or more complementarity
PT determining regions, useful for diagnosing and treating disorders
PT associated with angiogenesis, tumor growth and/or cancer metastasis.
XX
PS Example 1; SEQ ID NO 2; 232pp; English.
XX
CC This invention relates to a novel grafted antibody or its functional
CC fragment comprising one or more complementarity determining regions
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
CC acid (aa) substitution where the antibody has specific binding activity
CC for a cryptic collagen epitope. The growth of all solid tumours requires
CC new blood vessel growth, angiogenesis, inhibition of which is an approach
CC to limiting tumour growth. The invention may allow development of
CC therapeutics with a cytostatic activity as a collagen agonist or
CC antagonist. The invention is useful for diagnosing and treating disorders
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
CC present sequence is the partial amino acid sequence of the mouse anti-
CC cryptic collagen site antibody HUIV26 variable region light chain used
CC during the creation of the antibody of the invention.
XX
SQ Sequence 113 AA;
Query Match 89.9%; Score 545; DB 7; Length 113;

Best Local Similarity 92.9%; Pred. No. 3.1e-38;
Matches 105; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYG 63
Db 1 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPPKLLIYG 60

QY 64 DSGVPDRFTGSGSGTDFTLTISSSVQAEDLAVYYCQNDHIYPTTFGGGTKLEIK 116
Db 61 ESGVPDRFTGSGSGTDFTLIISVQAEDLAVYYCQNDHSYPYTFGGGTKLEIK 113

RESULT 3
ADV66167
ID ADV66167 standard; protein; 113 AA.
XX
AC ADV66167;
XX
DT 24-FEB-2005 (first entry)
XX
DE Human EpCAM-specific antibody light chain variable domain - SEQ ID 90.
XX
KW bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; tumor; cancer; cytostatic; light chain variable region.
XX
OS Unidentified.
XX
PN WO2004106383-A1.
XX
PD 09-DEC-2004.
XX
PF 26-MAY-2004; 2004WO-EP005687.
XX
PR 31-MAY-2003; 2003EP-00012133.
PR 31-MAY-2003; 2003EP-00012134.
XX
PA (MICR-) MICROMET AG.
XX
PI Kufer P, Berry M, Offner S, Brieschwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
XX
DR WPI; 2005-021271/02.
DR N-PSDB; ADV66166.
XX
PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.
XX
PS Claim 10; SEQ ID NO 90; 227pp; English.
XX
CC The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents an antibody
CC light chain variable domain that is specific for human EpCAM.
XX
SQ Sequence 113 AA;
Query Match 89.9%; Score 545; DB 9; Length 113;
Best Local Similarity 92.0%; Pred. No. 3.1e-38;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYG 63
Db 1 ELVMTQSPSSLVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPPKLLIYG 60

QY 64 DSGVPDRFTGSGSGTDFTLTISSSVQAEDLAVYYCQNDHIYPTTFGGGTKLEIK 116
Db 61 ESGVPDRFTGSGSGTDFTLTISSSVQAEDLAVYYCQNDHSYPYTFGGGTKLEIK 113



AC ADZ83445;  
XX  
DT 14-JUL-2005 (first entry)  
XX  
DE CD3 specific binding construct SEQ ID NO 67.  
XX  
KW neoplasm; inflammation; immune disorder; infection; allergy;  
KW graft versus host disease; Cytostatic; Antiinflammatory;  
KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.  
XX  
OS Synthetic.  
XX  
PN WO2005040220-A1.  
XX  
PD 06-MAY-2005.  
XX  
PF 15-OCT-2004; 2004WO-EP011646.  
XX  
PR 16-OCT-2003; 2003EP-00023581.  
XX  
PA (MICR-) MICROMET AG.  
XX  
PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;  
PI Carr FJ, Hamilton AA, Williams S;  
XX  
DR WPI; 2005-333494/34.  
DR N-PSDB; ADZ83444.  
XX  
PT New cytotoxically active CD3 specific binding construct comprises a first  
PT domain specifically binding to human CD3 and an Ig-derived second binding  
PT domain, useful for treating, preventing, or ameliorating, e.g.  
PT proliferative disease.  
XX  
PS Claim 20; SEQ ID NO 67; 639pp; English.  
XX  
CC The invention relates to a cytotoxically active CD3 specific binding  
CC construct comprises a first domain specifically binding to human CD3 and  
CC an Ig-derived second binding domain. The CD3 specific binding construct  
CC above or the construct produced by the process, nucleic acid molecule,  
CC vector, or host is useful for the preparation of a pharmaceutical  
CC composition for the prevention, treatment, or amelioration of a  
CC proliferative disease, a tumor, an inflammatory disease, an immunological  
CC disorder, an autoimmune disease, an infectious disease, viral disease,  
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
CC construct is useful for treating, preventing, or ameliorating  
CC proliferative disease, a tumor, an inflammatory disease, an immunological  
CC disorder, an autoimmune disease, an infectious disease, viral disease,  
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
CC host-versus-graft diseases. The present sequence represents the amino  
CC acid sequence of a CD3 specific binding construct.  
XX  
SQ Sequence 497 AA;  
  
Query Match 89.9%; Score 545; DB 9; Length 497;  
Best Local Similarity 92.0%; Pred. No. 1.3e-37;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
  
QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 385 ELVMTQSPSSLVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 444  
  
QY 64 DSGVPDRFTGSGGTDFTLTISVQAE DLAVYYCQNDHIYPYTFGGG TKLEIK 116  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 445 ESGVPDRFTGSGGTDFTLTISVQAE DLAVYYCQNDYSYPYTFGGG TKLEIK 497  
  
RESULT 7  
ADV66137  
ID ADV66137 standard; protein; 500 AA.  
XX  
AC  
XX ADV66137;  
XX

DT 24-FEB-2005 (first entry)  
XX  
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 60.  
XX  
KW bispecific single chain antibody; epithelial cell adhesion molecule;  
KW EpCAM; CD3; tumor; cancer; cytostatic.  
XX  
OS Unidentified.  
XX  
PN WO2004106383-A1.  
XX  
PD 09-DEC-2004.  
XX  
PF 26-MAY-2004; 2004WO-EP005687.  
XX  
PR 31-MAY-2003; 2003EP-00012133.  
PR 31-MAY-2003; 2003EP-00012134.  
XX  
PA (MICR-) MICROMET AG.  
XX  
PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;  
PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;  
XX  
DR WPI; 2005-021271/02.  
DR N-PSDB; ADV66136.  
XX  
PT New pharmaceutical composition having a bispecific single chain antibody  
PT construct, useful for preventing, treating or ameliorating a tumorous  
PT disease, such as an epithelial or minimal residual cancer.  
XX  
PS Claim 12; SEQ ID NO 60; 227pp; English.  
XX  
CC The invention comprises a composition that contains a bispecific single  
CC chain antibody consisting of at least two domains, where one of domains  
CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the  
CC second domain binds to human CD3 antigen. The bispecific antibody  
CC construct of the invention is useful for the prevention, treatment or  
CC amelioration of a tumorous disease, such as an epithelial or minimal  
CC residual cancer. The present amino acid sequence represents a bispecific  
CC single chain antibody of the invention.  
XX  
SQ Sequence 500 AA;  
  
Query Match 89.9%; Score 545; DB 9; Length 500;  
Best Local Similarity 92.0%; Pred. No. 1.4e-37;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
  
QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 382 ELVMTQSPSSLVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 441  
  
QY 64 DSGVPDRFTGSGGTDFTLTISVQAE DLAVYYCQNDHIYPYTFGGG TKLEIK 116  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 442 ESGVPDRFTGSGGTDFTLTISVQAE DLAVYYCQNDYSYPYTFGGG TKLEIK 494  
  
RESULT 8  
ADV66133  
ID ADV66133 standard; protein; 503 AA.  
XX  
AC ADV66133;  
XX  
DT 24-FEB-2005 (first entry)  
XX  
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 56.  
XX  
KW bispecific single chain antibody; epithelial cell adhesion molecule;  
KW EpCAM; CD3; tumor; cancer; cytostatic.  
XX  
OS Unidentified.  
XX  
PN WO2004106383-A1.  
XX





CC The invention relates to a cytotoxically active CD3 specific binding  
CC construct comprises a first domain specifically binding to human CD3 and  
CC an Ig-derived second binding domain. The CD3 specific binding construct  
CC above or the construct produced by the process, nucleic acid molecule,  
CC vector, or host is useful for the preparation of a pharmaceutical  
CC composition for the prevention, treatment, or amelioration of a  
CC proliferative disease, a tumor, an inflammatory disease, an immunological  
CC disorder, an autoimmune disease, an infectious disease, viral disease,  
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding  
CC construct is useful for treating, preventing, or ameliorating  
CC proliferative disease, a tumor, an inflammatory disease, an immunological  
CC disorder, an autoimmune disease, an infectious disease, viral disease,  
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or  
CC host-versus-graft diseases. The present sequence represents the amino  
CC acid sequence of deimmunized construct 4-1xanti-CD3.

XX Sequence 515 AA;

Query Match 89.9%; Score 545; DB 9; Length 515;  
Best Local Similarity 92.0%; Pred. No. 1.4e-37;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63  
Db 20 ELVMTQSPSSLSVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 79

QY 64 DSGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116  
Db 80 ESGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDYSYPYTFGGGTKLEIK 132

RESULT 11  
ADV66116  
ID ADV66116 standard; protein; 521 AA.  
XX ADV66116;  
AC  
XX  
XX  
DT 24-FEB-2005 (first entry)  
XX  
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 39.  
XX bispecific single chain antibody; epithelial cell adhesion molecule;  
KW EpCAM; CD3; tumor; cancer; cytostatic.  
KW  
XX Unidentified.  
XX  
XX WO2004106383-A1.  
PN  
XX  
PD 09-DEC-2004.  
XX  
PF 26-MAY-2004; 2004WO-EP005687.  
XX  
PR 31-MAY-2003; 2003EP-00012133.  
PR 31-MAY-2003; 2003EP-00012134.  
XX  
PA (MICR-) MICROMET AG.  
XX

PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;  
PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;  
XX WPI; 2005-021271/02.  
DR N-PSDB; ADV66115.  
XX  
PT New pharmaceutical composition having a bispecific single chain antibody  
PT construct, useful for preventing, treating or ameliorating a tumorous  
PT disease, such as an epithelial or minimal residual cancer.  
XX  
PS Claim 12; SEQ ID NO 39; 227pp; English.  
XX

CC The invention comprises a composition that contains a bispecific single  
CC chain antibody consisting of at least two domains, where one of domains  
CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the

CC second domain binds to human CD3 antigen. The bispecific antibody  
CC construct of the invention is useful for the prevention, treatment or  
CC amelioration of a tumorous disease, such as an epithelial or minimal  
CC residual cancer. The present amino acid sequence represents a bispecific  
CC single chain antibody of the invention.

XX Sequence 521 AA;

Query Match 89.9%; Score 545; DB 9; Length 521;  
Best Local Similarity 92.0%; Pred. No. 1.4e-37;  
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63  
Db 20 ELVMTQSPSSLSVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 79

QY 64 DSGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116  
Db 80 ESGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDYSYPYTFGGGTKLEIK 132

RESULT 12  
AAB62864  
ID AAB62864 standard; protein; 114 AA.  
XX  
AC AAB62864;  
XX

DT 15-MAY-2001 (first entry)  
XX  
DE Anti-SAF-1 monoclonal antibody 13G3 kappa chain variable region protein.  
XX

KW Sialoadhesin factor-1; SAF-1; anti-SAF-1 monoclonal antibody; 13G3; 11G4;  
KW osteomyelitis; wound infection; sepsis; Listeria monocytogene;  
KW Salmonella; Leishmania; kappa chain variable region; mouse.

XX Mus musculus.

XX WO200112646-A1.

XX 22-FEB-2001.

PF 18-AUG-2000; 2000WO-US022663.

XX 19-AUG-1999; 99US-0149753P.

XX (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX

PI Erickson-Miller CL, Holmes SD, King AG, Taylor AH;

XX WPI; 2001-211197/21.  
DR N-PSDB; AAF62143.

XX  
PT New sialoadhesin factor-1 agonist antibody having the characteristic of  
PT monoclonal antibody 13G3 or 11G4 for treating osteomyelitis, deep seated  
PT wound infections and antibiotic resistant bacterial infections.

PS Claim 19; Fig 2; 43pp; English.

XX  
CC This invention relates to sialoadhesin factor-1 (SAF-1) monoclonal  
CC antibodies 13G3 and 11G4. A neutrophil-priming dose of SAF-1 agonist  
CC antibody or a pharmaceutical composition comprising the antibody is  
CC useful for treating or preventing an infectious disease state such as  
CC osteomyelitis, deep seated wound infections, sepsis, antibiotic resistant  
CC bacterial infection, viral infections and those involving intracellular  
CC pathogens and parasites such as Listeria monocytogenes, Salmonella and  
CC Leishmania in a mammal. Nucleic acid sequences encoding the variable  
CC light chain and heavy chain peptide sequences are useful for mutagenic  
CC introduction of specific changes within the nucleic acid sequences  
CC encoding the (complementarity determining regions) CDRs or framework  
CC regions, and for incorporation of the resulting modified or fusion  
CC nucleic acid sequence into a plasmid for expression. The CDR-encoding  
CC regions comprising silent mutations are used in construction of humanized



PI Pastan IH, Lee B, Jung S, Brinkmann U;  
XX WP1; 1995-036408/05.  
DR  
XX New ligand-binding polypeptide(s) - having a disulphide bond linking  
PT framework regions of first and second variable regions of ligand binding  
PT moieties.  
XX  
PS Disclosure; Page 53; 67pp; English.  
XX  
CC The polypeptide given in AAR68742 corresponds to the light chain of MAb  
CC McPC603. This MAb was used to generate a model of MAb B3(Fv), which has  
CC been used in the construction of disulfide bond-stabilized Fv fragments  
CC used as immunotoxins. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 113 AA;  
  
Query Match 88.4%; Score 536; DB 2; Length 113;  
Best Local Similarity 91.2%; Pred. No. 1.8e-37;  
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
  
QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63  
Db 1 DIVMTQSPSSLVSAGERVTMSCKSSQSLNSGNQKNFLAWYQQKPGQPPKLLIYGASTR 60  
  
QY 64 DSGVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116  
Db 61 ESGVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHSYPLTFGAGTKLEIK 113  
  
RESULT 15  
AAW58483  
ID AAW58483 standard; protein; 113 AA.  
XX  
AC AAW58483;  
XX  
DT 18-AUG-1998 (first entry)  
XX  
DE Murine MCPC antibody light chain variable domain.  
XX  
KW Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;  
KW depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;  
KW autoimmune disease; rheumatoid arthritis; type I diabetes.  
XX  
OS Mus sp.  
XX  
PN US5770196-A.  
XX  
PD 23-JUN-1998.  
XX  
PF 07-JUN-1995; 95US-00472788.  
XX  
PR 13-DEC-1991; 91US-00808464.  
PR 14-DEC-1992; 92WO-US010906.  
PR 23-JUN-1993; 93US-00082842.  
XX  
PA (XOMA ) XOMA CORP.  
XX  
PI Studnicka GM;  
XX  
DR WPI; 1998-376744/32.  
XX  
PT Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies with  
PT humanised variable regions.  
XX  
PS Disclosure; Col 43-44; 77pp; English.  
XX  
CC A method has been developed of depleting CD5+ cells in an animal. The  
CC method comprises administering a cytotoxic protein containing a modified  
CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig  
CC molecule or an immunoconjugate or fusion protein containing an anti-CD5  
CC Ig molecule, and where the modified Ig variable domain comprises at least  
CC one of (a) a modified light chain variable region (see AAW58478 or

CC AAW58480), and (b) a modified heavy chain variable region (see AAW58479  
CC or AAW58481), where AAW58478 and AAW58479 are humanised forms of the H65  
CC light and heavy chain variable domains with low risk amino acid  
CC substitutions [i.e. low risk of reducing antigen-binding specificity.]  
CC and AAW58480 and AAW58481 are humanised forms of the H65 light and heavy  
CC chain variable domains with moderate risk amino acid substitutions and  
CC are present in humanised H65 antibody he3 (ATCC HB 11206). The method is  
CC useful for treating autoimmune diseases, especially systemic lupus  
CC erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The  
CC present sequence represents the murine MCPC antibody light chain variable  
CC domain  
XX  
SQ Sequence 113 AA;  
  
Query Match 88.4%; Score 536; DB 2; Length 113;  
Best Local Similarity 91.2%; Pred. No. 1.8e-37;  
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
  
QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63  
Db 1 DIVMTQSPSSLVSAGERVTMSCKSSQSLNSGNQKNFLAWYQQKPGQPPKLLIYGASTR 60  
  
QY 64 DSGVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116  
Db 61 ESGVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHSYPLTFGAGTKLEIK 113  
  
Search completed: May 19, 2006, 17:40:05  
Job time : 138.333 secs



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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:40:37 ; Search time 22.0952 Seconds  
(without alignments)  
505.138 Million cell updates/sec

Title: US-09-889-936A-8  
Perfect score: 606  
Sequence: 1 SRGDIVMTQSPSSLVSAGE.....CQNDHIYPYTFGGGTKLEIK 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	542	89.4 135 2 S38807	Ig light chain V-J
2	536	88.4 112 2 F30538	Ig kappa chain V r
3	536	88.4 112 2 E30538	Ig kappa chain V r
4	531	87.6 113 2 PL0264	Ig kappa chain V r
5	520	85.8 108 2 E30535	Ig kappa chain V r
6	515	85.0 107 2 G30535	Ig kappa chain V r
7	512	84.5 107 2 F30535	Ig kappa chain V r
8	509	84.0 113 2 PL0263	Ig kappa chain V r
9	508	83.8 107 2 D30535	Ig kappa chain V r
10	508	83.8 107 2 B30535	Ig kappa chain V r
11	503	83.0 105 2 C30535	Ig kappa chain V r
12	495	81.7 220 2 A31790	Ig kappa chain V r
13	485	80.0 214 2 S68212	Ig kappa chain (Ma
14	473.5	78.1 112 2 S43103	Ig kappa chain V-J
15	473.5	78.1 113 2 PT0407	Ig light chain V r
16	473	78.1 145 2 PL0014	Ig kappa chain pre
17	472.5	78.0 118 2 PT0356	Ig kappa chain V r
18	470.5	77.6 112 2 PL0265	Ig kappa chain V r
19	469.5	77.5 112 2 S41393	Ig kappa chain V r
20	467.5	77.1 133 2 PS0023	Ig kappa chain pre
21	467	77.1 134 2 PC1214	Ig kappa chain pre
22	464.5	76.7 111 2 G30502	Ig kappa chain V r
23	462	76.2 111 2 S03304	Ig kappa chain V r
24	461	76.1 113 2 JC2270	PL7-6 antibody lig
25	461	76.1 113 2 A49260	antitumor monoclon
26	460.5	76.0 138 2 S26040	Ig kappa chain pre
27	460	75.9 240 2 S06084	Ig kappa chain pre
28	459.5	75.8 113 2 PT0408	Ig light chain V r
29	457	75.4 113 2 S30520	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S38807  
Ig light chain V-J region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S38807  
R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.  
Immunogenetics 36, 15-21, 1992  
A;Title: Molecular characterization of the variable regions of a mouse polyclonal IgG2b  
A;Reference number: S38807; MUID:92267566; PMID:1587549  
A;Accession: S38807  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-135 <SEQ>  
A;Cross-references: UNIPARC:UPI0000176CA6; EMBL:X59816  
A;Note: the authors translated the codon GGC for residue 1 as Ala and TGT for residue 21  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;38-118/Domain: immunoglobulin homology <IMM>

Query Match		89.4%;	Score 542;	DB 2;	Length 135;
Best Local Similarity		91.2%;	Pred. No. 8.7e-41;		
Matches	103;	Conservative	3;	Mismatches	7;
				Indels	0;
				Gaps	0;
Qy	3	GDIVMTQSPSSLVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQKPGQPPKLLIYGVEI	62		
Db	22	GDIVMTQSPSSLTVSAGEKVTMSCKSSQSLFNSGTQKNYLAWYQKPGQPPKLLIYGAST	81		
Qy	63	RDSGVPDRFTGSGSGTDTLTITISSVQAEDLAVYYCQNDHIYPYTFGGGKLEI	115		
Db	82	RESGVPDRFTGSGSGTDTLTITISSVQAEDLAVYYCQNDHSYPYTFGGGKLDI	134		

RESULT 2

F30538  
Ig kappa chain V region (253.15D10) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Feb-1989 #sequence\_revision 10-Feb-1989 #text\_change 21-Jan-2000  
C;Accession: F30538  
R;Claflin, J.L.; Berry, J.  
J. Immunol. 141, 4012-4019, 1988  
A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae  
A;Reference number: A30534; MUID:89035545; PMID:3141511  
A;Accession: F30538  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-112 <CLA>  
A;Cross-references: UNIPARC:UPI0000176CD5  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>











Db : ||||| : |||||  
61 ECGVDRFTGSGTDFTLTISSVQAEDLAVYYCKQSYNL-YTFGGTKLEIK 112

Search completed: May 19, 2006, 17:47:24  
Job time : 23.0952 secs

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November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:34:57 ; Search time 176.762 Seconds  
(without alignments)  
607.041 Million cell updates/sec

Title: US-09-889-936A-8  
Perfect score: 606  
Sequence: 1 SRGDIVMTQSPSSLSVSAGE.....CQNDHIYPYTFGGGTKLEIK 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	531	87.6	255	2 Q6KB05_MOUSE	Q6kb05 mus musculus
2	468	77.2	240	2 Q52L64_MOUSE	Q52l64 mus musculus
3	456	75.2	114	1 KV4A_HUMAN	P01625 homo sapien
4	454	74.9	134	1 KV4C_HUMAN	P06314 homo sapien
5	452.5	74.7	133	1 KV4B_HUMAN	P06313 homo sapien
6	410	67.7	121	1 KV40_HUMAN	P06312 homo sapien
7	402	66.3	136	1 KV5B_MOUSE	P01634 mus musculus
8	401	66.2	109	1 KV4D_HUMAN	P83593 homo sapien
9	398	65.7	114	1 KV1A_MOUSE	P01632 mus musculus
10	391	64.5	115	2 Q5F2I0_MOUSE	Q5f2i0 mus musculus
11	385	63.5	149	1 KV5A_MOUSE	P01633 mus musculus
12	382.5	63.1	109	2 Q9UL78_HUMAN	Q9ul78 homo sapien
13	381.5	63.0	129	1 KV3L_HUMAN	P18135 homo sapien
14	381.5	63.0	239	2 Q58EU8_MOUSE	Q58eu8 mus musculus
15	380.5	62.8	129	1 KV3H_HUMAN	P04207 homo sapien
16	380	62.7	236	2 Q6GMX8_HUMAN	Q6gmx8 homo sapien
17	378.5	62.5	129	1 KV3M_HUMAN	P18136 homo sapien
18	376.5	62.1	235	2 Q6GMV9_HUMAN	Q6gmv9 homo sapien
19	376.5	62.1	235	2 Q6GMW0_HUMAN	Q6gmw0 homo sapien
20	374.5	61.8	248	2 Q65ZQ7_9MURI	Q65zq7 mus sp. b3(
21	374	61.7	236	2 Q6PIL8_HUMAN	Q6pil8 homo sapien
22	374	61.7	240	2 Q6PIH6_HUMAN	Q6pih6 homo sapien
23	373.5	61.6	109	1 KV3B_HUMAN	P01620 homo sapien
24	373	61.6	111	2 Q920E9_MOUSE	Q920e9 mus musculus
25	372.5	61.5	109	1 KV3F_HUMAN	P01624 homo sapien
26	372	61.4	108	1 KV1M_HUMAN	P01605 homo sapien
27	371	61.2	108	1 KV1Y_HUMAN	P80362 homo sapien
28	371	61.2	111	1 KV3H_MOUSE	P01660 mus musculus
29	370.5	61.1	108	1 KV3A_HUMAN	P01619 homo sapien
30	370	61.1	108	1 KV5P_MOUSE	P01649 mus musculus
31	370	61.1	108	2 Q9UL70_HUMAN	Q9ul70 homo sapien

32	370	61.1	115	1 KV2A_HUMAN	P01614 homo sapien
33	369	60.9	108	2 Q8VIJ0_MOUSE	Q8vi0 mus musculus
34	369	60.9	236	2 Q6GMW1_HUMAN	Q6gmw1 homo sapien
35	368.5	60.8	219	2 Q65ZC0_MOUSE	Q65zc0 mus musculus
36	368	60.7	236	2 Q7Z3Y4_HUMAN	Q7z3y4 homo sapien
37	367.5	60.6	113	1 KV2G_MOUSE	P01631 mus musculus
38	367	60.6	108	2 Q9UL79_HUMAN	Q9ul79 homo sapien
39	367	60.6	108	2 Q9UL83_HUMAN	Q9ul83 homo sapien
40	367	60.6	111	1 KV3M_MOUSE	P01665 mus musculus
41	367	60.6	131	1 KV3I_MOUSE	P01661 mus musculus
42	367	60.6	238	2 Q66JS7_MOUSE	Q66js7 mus musculus
43	366.5	60.5	239	2 Q8NEK0_HUMAN	Q8nek0 homo sapien
44	366	60.4	108	1 KV1V_HUMAN	P04430 homo sapien
45	365.5	60.3	109	2 Q9UL85_HUMAN	Q9ul85 homo sapien

ALIGNMENTS

RESULT 1  
Q6KB05\_MOUSE  
ID Q6KB05\_MOUSE PRELIMINARY; PRT; 255 AA.  
AC Q6KB05;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE ScFv B8E5 protein (Fragment).  
GN Name=scFv B8E5;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Murioidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c;  
RX PubMed=15485827; DOI=10.1074/jbc.M407213200;  
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,  
RA Briand J.P., Hoebeke J.;  
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with  
monoclonal anti-M2 receptor antibody fragments.";  
RL J. Biol. Chem. 279:55697-55706(2004).  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AJ746180; CAG34081.1; -; Other\_DNA.  
DR HSSP; P01837; 1KCR.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR013106; V-set.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Immunoglobulin domain.  
FT NON\_TER 1  
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 87.6%; Score 531; DB 2; Length 255;  
Best Local Similarity 91.2%; Pred. No. 2.4e-48;  
Matches 103; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy	4	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVEIR 63
Db	137	DIVMAQSPSSLSVSAGEKVMCKSSQSLNSRNQKNYLAWYQKPGQSPKLLIYGASTR 196
Qy	64	DSGVPDRFTGSGSGTDTLTLTISSVQAEDLAVYYCONDHIYPYTFGGGTKLEIK 116
Db	197	ESGVPDRFTGSGSGTDTLTLTISSVQAEDLAVYYCONDHSYPLTFGAGTKLEIK 249

RESULT 2

Q52L64\_MOUSE  
ID Q52L64\_MOUSE PRELIMINARY; PRT; 240 AA.  
AC Q52L64;  
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 24-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Hypothetical protein.  
DE Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
CC -----  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; BC094049; AAH94049.1; -; mRNA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 240 AA; 26609 MW; CF8630CCC002E52C CRC64;

Query Match 77.2%; Score 468; DB 2; Length 240;  
Best Local Similarity 78.9%; Pred. No. 1.3e-41;  
Matches 90; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 3 GDIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPLLIYGVFI 62  
Db 20 GDIVMSQSPSSLVSGEKVTMSCKSSQSLLSYNQKNYLAWYQQKPGQSPKLLIYWAST 79  
QY 63 RDSGVPDRFTGSGSGTDFLTLTSSVQAEALVYYQNDHIYPTFTGGGTKLEIK 116  
Db 80 RESGVPDHFSGSGTDFLTLTSSVKAEDLALYYCQYYNYPLTFTGAGTKLDLR 133

RESULT 3  
KV4A\_HUMAN STANDARD; PRT; 114 AA.  
ID KV4A\_HUMAN  
AC P01625;  
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-1996, sequence version 2.  
DT 07-MAR-2006, entry version 50.  
DE Ig kappa chain V-IV region Len.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=76004342; PubMed=50995;  
RA Schneider M., Hileschmann N.;  
RT "The primary structure of a monoclonic immunoglobulin-L-chain of  
RT subgroup IV of the kappa type (Bence-Jones protein Len).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).  
RN [2]  
RP SEQUENCE REVISION TO 9.  
RA Salomon A.;  
RL Submitted (AUG-1996) to Swiss-Prot.  
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.  
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR PDB; 1EEQ; X-ray; A/B=1-114.  
DR PDB; 1EEU; X-ray; A/B=1-114.  
DR PDB; 1EFQ; X-ray; A=1-114.  
DR PDB; 1EK3; X-ray; A/B=1-101.  
DR PDB; 1LVE; X-ray; @=1-114.  
DR PDB; 2LVE; X-ray; @=1-114.  
DR PDB; 3LVE; X-ray; @=1-114.  
DR PDB; 4LVE; X-ray; A/B=1-114.  
DR PDB; 5LVE; X-ray; A=1-114.  
DR LinkHub; P01625; -.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;  
KW Immunoglobulin domain; Immunoglobulin V region.  
FT CHAIN 1 >114 Ig kappa chain V-IV region Len.  
FT Framework\_1. /FTID=PRO\_0000059768.  
FT REGION 1 23 Framework-1.  
FT REGION 24 40 Complementarity-determining-1.  
FT REGION 41 55 Framework-2.  
FT REGION 56 62 Complementarity-determining-2.  
FT REGION 63 94 Framework-3.  
FT REGION 95 101 Complementarity-determining-3.  
FT REGION 102 113 Framework-4.  
FT DISULFID 23 94 By similarity.  
FT NON TER 114 114  
FT STRAND 4 7  
FT STRAND 9 13  
FT TURN 15 16  
FT STRAND 17 17  
FT STRAND 19 27  
FT STRAND 30 31  
FT TURN 32 35

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FT STRAND 36 37
FT STRAND 39 44
FT TURN 46 47
FT STRAND 48 48
FT STRAND 51 55
FT TURN 56 58
FT STRAND 59 60
FT TURN 62 63
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 75
FT STRAND 76 83
FT HELIX 86 88
FT STRAND 90 96
FT STRAND 98 101
FT STRAND 103 104
FT STRAND 108 112
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 75.2%; Score 456; DB 1; Length 114;
Best Local Similarity 77.0%; Pred. No. 1e-40;
Matches 87; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR 60
QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db 61 ESGVPDRFSGSGSGTDFTLTISSLAQEDVAVYYCQYVSTPYSFGQGTKLEIK 113

RESULT 4
KV4C_HUMAN
ID KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-APR-1988, sequence version 1.
DT 07-MAR-2006, entry version 45.
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT probe.";
RL Nucleic Acids Res. 13:6531-6544 (1985).
RN [2]
RP SEQUENCE REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X02990; CAA26733.1; -; mRNA.
DR HSSP; P01625; 1LVE.
DR SMR; P06314; 21-134.
DR LinkHub; P06314; -.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR
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DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134
FT Ig kappa chain V-IV region B17.
FT /FTid=PRO_0000015183.
FT Framework-1.
FT REGION 21 43
FT REGION 44 60
FT REGION 61 75
FT REGION 76 82
FT REGION 83 114
FT REGION 115 121
FT REGION 122 133
FT DISULFID 43 114
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 74.9%; Score 454; DB 1; Length 134;
Best Local Similarity 75.4%; Pred. No. 2.1e-40;
Matches 86; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 3 GDIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFI 62
Db 20 GDIVMTQSPDLSAVSLGERATINCKSSQSIYSSDNKNYLAWYQQKPGQPPKLLIYWAST 79
QY 63 RDSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db 80 RESGVPDRFSGSGSGTDFTLTISSLAQEDVAVYYCQYVNLPTWTFGQGTKVEIK 133

RESULT 5
KV4B_HUMAN
ID KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1988, sequence version 1.
DT 07-MAR-2006, entry version 43.
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RA "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529 (1985).
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CC -----
DR EMBL; Z00022; CAA77317.1; -; Genomic_DNA.
DR PIR; A01904; K4HUJ1.
DR HSSP; P01625; 1LVE.
DR SMR; P06313; 21-133.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133
FT Ig kappa chain V-IV region JI.
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FT REGION 21 43 /FTId=PRO_0000015182.
FT REGION 44 60 Framework-1.
FT REGION 61 75 Complementarity-determining-1.
FT REGION 76 82 Framework-2.
FT REGION 83 114 Complementarity-determining-2.
FT REGION 115 122 Framework-3.
FT REGION 123 132 Complementarity-determining-3.
FT DISULFID 43 114 Framework-4.
FT NON TER 133 By similarity.
SQ SEQUENCE 133 AA; 14633 MW; 5FB3953066744AF4 CRC64;

Query Match 74.7%; Score 452.5; DB 1; Length 133;
Best Local Similarity 77.2%; Pred. No. 3e-40;
Matches 88; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 3 GDIVMTQSPSSLVSAGEKVTMSCKSSQSLNRSNQKNYLAWYQQKPGQPPKLLIYGVFI 62
Db 20 GDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWAST 79
QY 63 RDSGVPDRFTGSGSGTDFLTITSSVQAE DLAVYYCQNDHIYPYTFGGGKLEIK 116
Db 80 RESGVPDRFSGSGSGTDFLTITSSLQAE DLAVYYCQYDTIP-TFGGGTKVEIK 132

RESULT 6
KV40_HUMAN
ID KV40_HUMAN STANDARD; PRT; 121 AA.
AC P06312;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-JAN-1988, sequence version 1.
DT 07-MAR-2006, entry version 45.
DE Ig kappa chain V-IV region precursor (Fragment).
GN Name=IGKV4-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -!- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
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CC -----
DR EMBL; Z00023; CAA77318.1; -; Genomic_DNA.
DR PIR; A01902; K4HU.
DR HSSP; P01625; 1LVE.
DR SMR; P06312; 21-121.
DR Ensembl; ENSG00000153586; Homo sapiens.
DR HGNC; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 Ig kappa chain V-IV region.
FT /FTId=PRO_0000015181.
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FT REGION 21 43 Framework-1.
FT REGION 44 60 Complementarity-determining-1.
FT REGION 61 75 Framework-2.
FT REGION 76 82 Complementarity-determining-2.
FT REGION 83 114 Framework-3.
FT REGION 115 121 Complementarity-determining-3.
FT DISULFID 43 114 By similarity.
FT NON TER 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 67.7%; Score 410; DB 1; Length 121;
Best Local Similarity 76.5%; Pred. No. 9.6e-36;
Matches 78; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 3 GDIVMTQSPSSLVSAGEKVTMSCKSSQSLNRSNQKNYLAWYQQKPGQPPKLLIYGVFI 62
Db 20 GDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWAST 79
QY 63 RDSGVPDRFTGSGSGTDFLTITSSVQAE DLAVYYCQNDHIYP 104
Db 80 RESGVPDRFSGSGSGTDFLTITSSLQAE DLAVYYCQYYSTP 121

RESULT 7
KV5B_MOUSE
ID KV5B_MOUSE STANDARD; PRT; 136 AA.
AC P01634;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 50.
DE Ig kappa chain V-V region MOPC 21 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [2]
RP PROTEIN SEQUENCE OF 30-136.
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
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CC -----
DR EMBL; V00810; CAA24192.1; ALT_TERM; mRNA.
DR PIR; A93736; KVMS21.
DR PDB; 1IGC; X-ray; L=30-136.
DR Ensembl; ENSMUSG0000060300; Mus musculus.
DR LinkHub; P01634; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Signal.
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FT CHAIN 30 136 Ig kappa chain V-V region MOPC 21.
FT /FTId=PRO_0000015190.
FT REGION 30 52 Framework-1.
FT REGION 53 63 Complementarity-determining-1.
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FT	REGION	79	85	Complementarity-determining-2.	
FT	REGION	86	117	Framework-3.	
FT	REGION	118	126	Complementarity-determining-3.	
FT	REGION	127	136	Framework-4.	
FT	NON TER	136	136		
FT	STRAND	34	36		
FT	STRAND	38	38		
FT	STRAND	41	43		
FT	TURN	44	45		
FT	STRAND	48	53		
FT	STRAND	55	56		
FT	TURN	59	60		
FT	STRAND	62	67		
FT	TURN	69	70		
FT	STRAND	71	71		
FT	STRAND	74	78		
FT	TURN	79	81		
FT	STRAND	82	83		
FT	TURN	85	86		
FT	TURN	89	90		
FT	STRAND	93	95		
FT	STRAND	97	106		
FT	STRAND	109	109		
FT	TURN	110	111		
FT	STRAND	113	119		
FT	STRAND	121	124		
FT	STRAND	126	127		
SQ	SEQUENCE	136 AA; 14902 MW; 8CDD85113996D1C2	CRC64;		
Query Match					66.3%; Score 402; DB 1; Length 136;
Best Local Similarity					67.5%; Pred. No. 8e-35;
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Db	29	GNIVMTQSPKSMMSVGERVTLTKASENVV-----TYVSWYQKPEQSP	KLLIYGASN 82		
QY	63	RDSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCONDHYPYTFGGG	TKLEIK 116		
Db	83	RYTGVDPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGSYPYTFGGG	TKLEIK 136		
RESULT 8					
KV4D HUMAN					
ID	KV4D_HUMAN	STANDARD;	PRT;	109 AA.	
AC	P83593;				
DT	30-MAY-2003,	integrated into UniProtKB/Swiss-Prot.			
DT	30-MAY-2003,	sequence version 1.			
DT	07-MAR-2006,	entry version 23.			
DE	Ig kappa chain V-IV region STH (Fragment).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	PROTEIN SEQUENCE.				
RC	TISSUE=Abdominal adipose tissue;				
RX	MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;				
RA	Olsen K.E., Sletten K., Westermarck P.;				
RT	"Extended analysis of AL-amyloid protein from abdominal wall				
RT	subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";				
RL	Biochem. Biophys. Res. Commun. 245:713-716(1998).				
CC	-!- FUNCTION: May play an important role in fibrillogenesis.				
CC	-----				
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CC	-----				
DR	SMR; P83593; 1-109.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	InterPro; IPR013106; V-set.				
DR	Pfam; PF07686; V-set; 1.				
DR	SMART; SM00409; IG; 1.				
DR	SMART; SM00406; IGv; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KW	Direct protein sequencing; Immunoglobulin domain;				
KW	Immunoglobulin V region.				
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FT					/FTid=PRO_0000059769.
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FT	REGION	24	40		Complementarity-determining-1.
FT	REGION	41	55		Framework-2.
FT	REGION	56	62		Complementarity-determining-2.
FT	REGION	63	94		Framework-3.
FT	REGION	95	101		Complementarity-determining-3.
FT	REGION	102	109		Framework-4.
FT	DISULFID	23	94		By similarity.
FT	UNSURE	23	23		
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FT	NON TER	109	109		
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Matches					77; Conservative 10; Mismatches 22; Indels 0; Gaps 0;
QY	4	DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQP	KLLIYGVIR 63		
Db	1	DIVMTQSPDSLVSLSGERATINCRSSQSVLYSSNNKNYLAWYQKPGQ	APKLLFSWASTR 60		
QY	64	DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCONDHYPYTFGGG	TK 112		
Db	61	ESGVPDRFSGSGSGTDFLTIPGLQAEDVAVYYCQYRIPYTFGGQ	AK 109		
RESULT 9					
KV1A MOUSE					
ID	KV1A_MOUSE	STANDARD;	PRT;	114 AA.	
AC	P01632;				
DT	21-JUL-1986,	integrated into UniProtKB/Swiss-Prot.			
DT	21-JUL-1986,	sequence version 1.			
DT	07-MAR-2006,	entry version 44.			
DE	Ig kappa chain V-I region S107A.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muroidea; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE [MRNA].				
RX	MEDLINE=81241357; PubMed=6788890; DOI=10.1084/jem.153.5.1366;				
RA	Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;				
RT	"Nucleic acid and protein sequences of phosphocholine-binding light				
RT	chains.";				
RL	J. Exp. Med. 153:1366-1370(1981).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE [MRNA] OF 1-113.				
RX	MEDLINE=89035545; PubMed=3141511;				
RA	Claflin J.L., Berry J.;				
RT	"Genetics of the phosphocholine-specific antibody response to				
RT	Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are				
RT	dominantly selected.";				
RL	J. Immunol. 141:4012-4019(1988).				
CC	-!- FUNCTION: Anti-phosphocholine antibody.				
CC	-----				
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CC	-----				
DR	EMBL; U29423; AAC00033.1; -; mRNA.				
DR	PIR; A01915; KVMS7A.				
DR	HSSP; Q9ERZ9; 2AP2.				
DR	SMR; P01632; 1-114.				
DR	Ensembl; ENSMUSG000000052500; Mus musculus.				

DR MGI; MGI:3577282; U29423.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain; Immunoglobulin V region.  
FT CHAIN 1 >114  
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FT REGION 24 40  
FT REGION 41 55  
FT REGION 56 62  
FT REGION 63 94  
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FT REGION 104 113  
FT DISULFID 23 94  
FT NON\_TER 114 114  
SQ SEQUENCE 114 AA; 12717 MW; 32008EC8E9DBE67B CRC64;  
  
Query Match 65.7%; Score 398; DB 1; Length 114;  
Best Local Similarity 68.1%; Pred. No. 1.7e-34;  
Matches 77; Conservative 15; Mismatches 21; Indels 0; Gaps 0;  
  
QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63  
Db 1 DIVMTQSPFLAVTASKKVTISCTASESLYSSKHVHYLAWYQKKPEQSPKLLIYGASNR 60  
  
QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAE DLAVVYCQNDHIYPYTFGGGTKLEIK 116  
Db 61 YIGVPDRFTGSGSGTDFTLTISSVQVEDLTHYCAQFYSYPLTFGGAGTKLELK 113  
  
RESULT 10  
Q5F2I0 MOUSE  
ID Q5F2I0\_MOUSE PRELIMINARY; PRT; 115 AA.  
AC Q5F2I0;  
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.  
DT 15-MAR-2005, sequence version 1.  
DT 07-FEB-2006, entry version 6.  
DE Kappa light chain variable region (Fragment).  
GN Name=IgG1 anti-TS1 VL;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Murioidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22716456; PubMed=12833571; DOI=10.1002/jmr.617;  
RA Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;  
RT "Studies of the interactions between the anticytokeratin 8 monoclonal  
RT antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1.";  
RL J. Mol. Recognit. 16:157-163(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22716456; PubMed=12833571; DOI=10.1002/jmr.617;  
RA Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;  
RT "Studies of the interactions between the anticytokeratin 8 monoclonal  
RT antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1.";  
RL J. Mol. Recognit. 16:157-163(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Erlandsson A.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBBJ databases.  
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CC -----  
DR EMBL; AJ884575; CAI56337.1; -; mRNA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR013106; V-set.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.

KW Immunoglobulin domain.  
FT NON\_TER 1 1  
FT NON\_TER 115 115  
SQ SEQUENCE 115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;  
  
Query Match 64.5%; Score 391; DB 2; Length 115;  
Best Local Similarity 68.4%; Pred. No. 9.9e-34;  
Matches 78; Conservative 14; Mismatches 20; Indels 2; Gaps 2;  
  
QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63  
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QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAE DLAVVYCQNDHIYPYTFGGGTKLEIK 116  
Db 60 FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPPYTFGGGTKLEMK 113  
  
RESULT 11  
KVSA MOUSE  
ID KVSA\_MOUSE STANDARD; PRT; 149 AA.  
AC P01633;  
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
DT 21-JUL-1986, sequence version 1.  
DT 07-MAR-2006, entry version 45.  
DE Ig kappa chain V-V region MPC11 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Murioidea; Muridae; Murinae; Mus.  
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RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-71.  
RX MEDLINE=83001944; PubMed=6288267; DOI=10.1016/0092-8674(82)90184-2;  
RA Kelley D.E., Coleclough C., Perry R.P.;  
RT "Functional significance and evolutionary development of the 5'-  
RT terminal regions of immunoglobulin variable-region genes.";  
RL Cell 29:681-689(1982).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 41-149.  
RX MEDLINE=80176554; PubMed=6245773;  
RA Rabbitts T.H., Hamlyn P.H., Matthysens G., Roe B.A.;  
RT "The variability, arrangement, and rearrangement of immunoglobulin  
RT genes.";  
RL Can. J. Biochem. 58:176-187(1980).  
RN [3]  
RP PROTEIN SEQUENCE OF 30-149.  
RX MEDLINE=78186617; PubMed=418775;  
RA Smith G.P.;  
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse  
RT myeloma MPC 11.";  
RL Biochem. J. 171:337-347(1978).  
CC -!- MISCELLANEOUS: The mature chain has 12 additional residues at its  
CC amino end, due to a tandem duplication of 36 nucleotides after the  
CC codon for residue 36. Residue 42 corresponds to the N-terminal  
CC residue of typical kappa chains.  
CC -----  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; J00561; AAA38776.1; -; Genomic\_DNA.  
DR PIR; A90823; KVMS11.  
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DR Ensembl; ENSMUSG00000061362; Mus musculus.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR InterPro; IPR013106; V-set.  
DR Pfam; PF07686; V-set; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.



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RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy." ;
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISBASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
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DR PIR; PLO022; K3HUHA.
DR HSSP; P01625; 1EEQ.
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DR Ensembl; ENSG00000169769; Homo sapiens.
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DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
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DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 12.
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GN Name=Igk-C;
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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
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RC STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung.
RC MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II; TISSUE=Mammary tumor metastatized to lung.
RC MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
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DR EMBL; BC091750; AAH91750.1; -; mRNA.
DR SMR; Q58EU8; 21-239.
DR MGI; MGI:96495; Igk-C.
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DR InterPro; IPR007110; Ig-like.
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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; C1-set; 1.
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DR SMART; SM00407; IGc1; 1.
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DT 01-NOV-1990, sequence version 2.
DT 07-MAR-2006, entry version 43.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OX NCBI_TaxID=9606;
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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:46:56 ; Search time 33.6032 Seconds  
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Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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9	536	88.4	Sequence 2, Appli
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ALIGNMENTS

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US-08-467-420A-45  
; Sequence 45, Application US/08467420A  
; Patent No. 5683892  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P. O. Box 1539-UW2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939  
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; OPERATING SYSTEM: PC-DOS/MS-DOS  
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; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/363131  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50282  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270-5024  
; TELEFAX: 610 270-5090  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
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; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P. O. Box 1539-UW2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939  
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; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50282  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270-5024  
; TELEFAX: 610 270-5090  
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US-08-470-110A-45

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; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; STREET: P.O. Box 1539-UW2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
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; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/363131  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50503  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5024  
; TELEFAX: 610-270-5090  
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US-08-667-769A-45  
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; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P. O. Box 1539-UW2220  
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; APPLICATION NUMBER: US/08/470,110  
; FILING DATE:  
; APPLICATION NUMBER: US 08/363131  
; FILING DATE: 23-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
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US-08-940-371-45

Query Match 89.3%; Score 541; DB 1; Length 113;  
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Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVFIR 63  
Db 1 ELVMTQSPSSLVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGQPPKLLIYGASTR 60  
Qy 64 DSGVPDRFTGSGGTDFTLTISVQAE DLAVYYCQNDHIYPYTFGGGTKLEIK 116  
Db 61 ESGVPDRFTGSGGTDFTLTISVQAE DLAVYYCQNDHSPFTFGSGTKLEIK 113

RESULT 5  
US-08-637-647-45  
; Sequence 45, Application US/08637647  
; Patent No. 6129913  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P. O. Box 1539-UW2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/637,647  
; FILING DATE: 19-JUN-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/363,131  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50282  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270-5024  
; TELEFAX: 610 270-5090  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-637-647-45

Query Match 89.3%; Score 541; DB 2; Length 113;  
Best Local Similarity 91.2%; Pred. No. 2.2e-42;  
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVFIR 63  
Db 1 ELVMTQSPSSLVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGQPPKLLIYGASTR 60  
Qy 64 DSGVPDRFTGSGGTDFTLTISVQAE DLAVYYCQNDHIYPYTFGGGTKLEIK 116  
Db 61 ESGVPDRFTGSGGTDFTLTISVQAE DLAVYYCQNDHSPFTFGSGTKLEIK 113

RESULT 6  
US-10-700-740-45  
; Sequence 45, Application US/10700740  
; Patent No. 6946130  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.



; Appelbaum, Edward R.
; Chaiken, Irwin M.
; Cook, Richard M.
; Gross, Mitchell S.
; Holmes, Stephen D.
; McMillan, Lynette J.
; Theisen, Timothy W.
;
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; Treatment of IL5 Mediated Disorders
;
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/700,740
; FILING DATE: 04-No. 6946130-2003
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
;
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-700-740-45
Query Match 89.3%; Score 541; DB 2; Length 113;
Best Local Similarity 91.2%; Pred. No. 2.2e-42;
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
: :
Db 1 ELVMTQSPSSLSVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 60

Qy 64 DSGVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
: :
Db 61 ESGVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHSYPFTFGSGTKLEIK 113

RESULT 7
PCT-US95-17082A-45
; Sequence 45, Application PC/TUS9517082A
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.

; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; Treatment of IL5 Mediated Disorders
;
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17082A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
;
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-17082A-45
Query Match 89.3%; Score 541; DB 5; Length 113;
Best Local Similarity 91.2%; Pred. No. 2.2e-42;
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
: :
Db 1 ELVMTQSPSSLSVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 60

Qy 64 DSGVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
: :
Db 61 ESGVPDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHSYPFTFGSGTKLEIK 113

RESULT 8
US-08-077-252B-4
; Sequence 4, Application US/08077252B
; Patent No. 5747654
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Lee, Byungkook
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Brinkmann, Ulrich
; TITLE OF INVENTION: Recombinant Disulfide-Stabilized
; Polypeptide Fragments Having Binding Specificity
; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/077,252B  
; FILING DATE: 14-JUN-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 15280-152  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..113  
; OTHER INFORMATION: /note= "Monoclonal antibody McPC603  
; OTHER INFORMATION: Light chain variable region (V-L)"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..23  
; OTHER INFORMATION: /label= FR1  
; OTHER INFORMATION: /note= "Framework Region 1 (FR1)"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 24..40  
; OTHER INFORMATION: /label= CDR1  
; OTHER INFORMATION: /note= "Complementarity Determining  
; OTHER INFORMATION: Region 1 (CDR1)"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 41..55  
; OTHER INFORMATION: /label= FR2  
; OTHER INFORMATION: /note= "Framework Region 2 (FR2)"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 49  
; OTHER INFORMATION: /note= "Light chain variable region Pro  
; OTHER INFORMATION: residue that can be changed to Cys,  
; OTHER INFORMATION: paired with Heavy chain variable region  
; OTHER INFORMATION: position 114 Ala residue change to Cys,  
; OTHER INFORMATION: for possible S2 site interchain  
; OTHER INFORMATION: disulfide bond"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 56..62  
; OTHER INFORMATION: /label= CDR2  
; OTHER INFORMATION: /note= "Complementarity Determining  
; OTHER INFORMATION: Region 2 (CDR2)"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 63..94  
; OTHER INFORMATION: /label= FR3  
; OTHER INFORMATION: /note= "Framework Region 3 (FR3)"  
; FEATURE:  
; NAME/KEY: Modified-site

; LOCATION: 93  
; OTHER INFORMATION: /note= "V-L93 Ser to Tyr mutation site  
; OTHER INFORMATION: (pseudo-symmetrically related to V-H97  
; OTHER INFORMATION: Ser to Tyr mutation site in Heavy  
; OTHER INFORMATION: chain variable region)"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 95..103  
; OTHER INFORMATION: /label= CDR3  
; OTHER INFORMATION: /note= "Complementarity Determining  
; OTHER INFORMATION: Region 3 (CDR3)"  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 104..109  
; OTHER INFORMATION: /label= FR4  
; OTHER INFORMATION: /note= "Framework Region 4 (FR4)"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 106  
; OTHER INFORMATION: /note= "Light chain variable region Ala  
; OTHER INFORMATION: residue that can be changed to Cys,  
; OTHER INFORMATION: paired with Heavy chain variable region  
; OTHER INFORMATION: position 144 Arg residue change to Cys,  
; OTHER INFORMATION: for possible S1 site interchain  
; OTHER INFORMATION: disulfide bond"  
; US-08-077-252B-4  
; Query Match 88.4%; Score 536; DB 1; Length 113;  
; Best Local Similarity 91.2%; Pred. No. 6.3e-42;  
; Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
; QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVFIR 63  
; Db 1 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSGNQKNFLAWYQKPGQPPKLLIYGASTR 60  
; QY 64 DSGVPDRFTGSGSGTDFTLTISVQAEDLAVYYQNDHIYPYTFGGGTKLEIK 116  
; Db 61 ESGVPDRFTGSGSGTDFTLTISVQAEDLAVYYQNDHSYPLTFGAGTKLEIK 113  
; RESULT 9  
; US-08-107-669D-2  
; Sequence 2, Application US/08107669D  
; Patent No. 5766886  
; GENERAL INFORMATION:  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
; STREET: 1100 New York Ave., N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: United States of America  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/107,669D  
; FILING DATE: 13-AUG-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: PCT/US92/10906  
; FILING DATE: 14-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/808,464  
; FILING DATE: 13-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michele A. Cimbalà  
; REGISTRATION NUMBER: 33,851

```

; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-2

Query Match      88.4%; Score 536; DB 1; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLNSGNQKNFLAWYQQKPGQPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db 61 ESGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDHSDSYPLTFGAGTKLEIK 113

RESULT 10
US-08-472-788A-2
; Sequence 2, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-788A-2
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Query Match      88.4%; Score 536; DB 1; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLNSGNQKNFLAWYQQKPGQPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db 61 ESGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDHSDSYPLTFGAGTKLEIK 113

RESULT 11
US-08-477-531B-2
; Sequence 2, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; MOLECULE TYPE: protein
US-08-477-531B-2

Query Match      88.4%; Score 536; DB 1; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLNSGNQKNFLAWYQQKPGQPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db 61 ESGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDHSDSYPLTFGAGTKLEIK 113
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RESULT 12
US-08-082-842A-2
; Sequence 2, Application US/08082842A
; Patent No. 5869619
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,842A
; FILING DATE: 23-JUN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-082-842A-2

Query Match      88.4%; Score 536; DB 1; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGQPPKLLIYGVFIR 63
Db      1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLNSGNQKNFLAWYQOKPGQPPKLLIYGASTR 60

QY      64 DSGVDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db      61 ESGVDRFTGSGSGTDFTLTISVQAEDLAVYYCQNDHYSYPLTFGAGTKLEIK 113

RESULT 13
US-09-002-753A-4
; Sequence 4, Application US/09002753A
; Patent No. 6147203
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Lee, Byungkook
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Brinkmann, Ulrich
; TITLE OF INVENTION: Recombinant Disulfide-Stabilized
; POLYPEPTIDE FRAGMENTS HAVING BINDING SPECIFICITY
; NUMBER OF SEQUENCES: 23
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,753A
; FILING DATE: 05-JAN-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,252
; FILING DATE: 14-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-152100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..113
; OTHER INFORMATION: /note= "Monoclonal antibody McPC603
; OTHER INFORMATION: Light chain variable region (V-L)"
; FEATURE:
; NAME/KEY: Region
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; OTHER INFORMATION: /note= "Framework Region 1 (FR1)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 24..40
; OTHER INFORMATION: /label= CDR1
; OTHER INFORMATION: /note= "Complementarity Determining
; OTHER INFORMATION: Region 1 (CDR1)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 41..55
; OTHER INFORMATION: /label= FR2
; OTHER INFORMATION: /note= "Framework Region 2 (FR2)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 56..62
; OTHER INFORMATION: /label= CDR2
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; OTHER INFORMATION: Region 2 (CDR2)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 63..94
; OTHER INFORMATION: /label= FR3
; OTHER INFORMATION: /note= "Framework Region 3 (FR3)"
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; NAME/KEY: Region
; LOCATION: 95..103
; OTHER INFORMATION: /label= CDR3
; OTHER INFORMATION: /note= "Complementarity Determining
; OTHER INFORMATION: Region 3 (CDR3)"
; FEATURE:
; NAME/KEY: Region
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; LOCATION: 104..109
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; OTHER INFORMATION: /note= "Framework Region 4 (FR4)"
US-09-002-753A-4

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Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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Db 61 ESGVPDRFTGSGSGTDFLTITSSVQAEDLAVYYCQNDHSYPLTFGAGTKLEIK 113

RESULT 14
US-09-657-274-4
; Sequence 4, Application US/09657274
; Patent No. 6558672
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; Lee, Byungkook
; Jung, Sun-Hee
; Brinkmann, Ulrich
; TITLE OF INVENTION: Recombinant Disulfide-Stabilized
; Polypeptide Fragments Having Binding Specificity
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/657,274
; FILING DATE: 07-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/002,753
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-152100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..113
; OTHER INFORMATION: /note= "Monoclonal antibody McPC603
; Light chain variable region (V-L)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..23
; OTHER INFORMATION: /label= FR1
; /note= "Framework Region 1 (FR1)"
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; Region 1 (CDR1)"
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; NAME/KEY: Region
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; OTHER INFORMATION: /label= CDR2
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; LOCATION: 63..94
; OTHER INFORMATION: /label= FR3
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; LOCATION: 95..103
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; /note= "Framework Region 4 (FR4)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-657-274-4

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Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNLRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
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QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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Db 61 ESGVPDRFTGSGSGTDFLTITSSVQAEDLAVYYCQNDHSYPLTFGAGTKLEIK 113

RESULT 15
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; Sequence 4, Application PC/TUS9406687
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant Disulfide-Stabilized
; TITLE OF INVENTION: Polypeptide Fragments Having Binding Specificity
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06687
; FILING DATE: 14-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..23
; OTHER INFORMATION: /label= FR1
; OTHER INFORMATION: /note= "Framework Region 1"
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; NAME/KEY: Region
; LOCATION: 24..40
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; OTHER INFORMATION: /note= "Complementarity Determining Region"
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; NAME/KEY: Region
; LOCATION: 41..55
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; OTHER INFORMATION: /note= "Framework Region 2"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 49
; OTHER INFORMATION: /note= "Residue that can be changed
; OTHER INFORMATION: to Cys fro possible interchain disulfide bond."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 56..62
; OTHER INFORMATION: /label= CDR2
; OTHER INFORMATION: /note= "Complementarity Determining Region 2"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 63..94
; OTHER INFORMATION: /label= FR3
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; NAME/KEY: Region
; LOCATION: 95..103
; OTHER INFORMATION: /label= CDR3
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; LOCATION: 104..113
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; OTHER INFORMATION: /note= "Framework Region 4"
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; LOCATION: 106
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; OTHER INFORMATION: to a Cys for possible interchain disulfide bond."
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; NAME/KEY: Modified-site
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PCT-US94-06687-4
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Query Match      88.4%; Score 536; DB 5; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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Qy      64 DSGVPDRFTGSGGTDFTLTISVQAEEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db      :|||||
Db      61 ESGVPDRFTGSGGTDFTLTISVQAEEDLAVYYCQNDHSYPLTFGAGTKLEIK 113
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 17:47:39 ; Search time 114.159 Seconds  
(without alignments)  
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Sequence: 1 SRGDIVMTQSPSSLVSAGE.....CQNDHIYPYTFGGGTKLEIK 116

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Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	545	89.9	113	3	US-09-995-529-2
2	545	89.9	113	3	US-09-995-529-2
3	541	89.3	113	4	US-10-144-644-45
4	541	89.3	113	4	US-10-700-740-45
5	541	89.3	113	6	US-11-076-395-45
6	536	88.4	113	4	US-10-340-189-2
7	536	88.4	113	4	US-10-325-696-2
8	536	88.4	113	6	US-11-133-775-2
9	536	88.4	115	5	US-10-700-632-68
10	535	88.3	113	4	US-10-144-644-46
11	535	88.3	113	4	US-10-700-740-46
12	535	88.3	113	6	US-11-076-395-46
13	526	86.8	113	4	US-10-144-644-16
14	526	86.8	113	4	US-10-700-740-16
15	526	86.8	113	6	US-11-076-395-16
16	526	86.8	678	6	US-11-202-507A-11
17	526	86.8	679	6	US-11-202-507A-5
18	525	86.6	482	4	US-10-345-618-16
19	523	86.3	118	5	US-10-491-653-148
20	520	85.8	263	5	US-10-512-184-29
21	518	85.5	115	3	US-09-998-831-9
22	518	85.5	115	4	US-10-373-561-9
23	518	85.5	115	5	US-10-738-404-9
24	516	85.1	113	4	US-10-160-506-71
25	516	85.1	113	4	US-10-160-506-91
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31	516	85.1	113	4	US-10-160-505-91	Sequence 91, Appl
32	516	85.1	113	6	US-11-218-813-71	Sequence 71, Appl
33	516	85.1	113	6	US-11-218-813-91	Sequence 91, Appl
34	513	84.7	258	4	US-10-239-656-59	Sequence 59, Appl
35	513	84.7	259	4	US-10-239-656-53	Sequence 53, Appl
36	513	84.7	378	5	US-10-743-697-1	Sequence 1, Appli
37	510	84.2	113	5	US-10-700-632-71	Sequence 71, Appl
38	510	84.2	258	4	US-10-239-656-71	Sequence 71, Appl
39	510	84.2	255	4	US-10-239-656-79	Sequence 79, Appl
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41	504	83.2	113	4	US-10-144-644-21	Sequence 21, Appl
42	504	83.2	113	4	US-10-700-740-21	Sequence 21, Appl
43	504	83.2	113	6	US-11-076-395-21	Sequence 21, Appl
44	495	81.7	115	5	US-10-700-632-64	Sequence 64, Appl
45	495	81.7	456	4	US-10-634-862-11	Sequence 11, Appl

ALIGNMENTS

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; Sequence 2, Application US/09995529  
; Publication No. US20030099655A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Tang, Ying  
; TITLE OF INVENTION: Humanized Collagen Antibodies and  
; TITLE OF INVENTION: Related Methods  
; FILE REFERENCE: P-IX 4976  
; CURRENT APPLICATION NUMBER: US/09/995,529  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-995-529-2

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Best Local Similarity	92.9%;	Pred. No. 2.9e-41;		
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Indels	0;	Gaps	0;	
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QY	64	DSGVPDRFTGSGSGTDFTLT	TISSVQAEDLAVYCONDHIYPYTFGGG	TKLEIK 116
Db	61	ESGVPDRFTGSGSGTDFTLT	LISSVQAEDLAVYCONDHSYPYTFGGG	TKLEIK 113
RESULT 2				
US-09-995-529-2				
; Sequence 2, Application US/09995529				
; Publication No. US20040091482A9				
; GENERAL INFORMATION:				
; APPLICANT: Watkins, Jeffrey D.				
; APPLICANT: Huse, William D.				
; APPLICANT: Tang, Ying				
; TITLE OF INVENTION: Humanized Collagen Antibodies and				
; TITLE OF INVENTION: Related Methods				
; FILE REFERENCE: P-IX 4976				
; CURRENT APPLICATION NUMBER: US/09/995,529				
; CURRENT FILING DATE: 2001-11-26				
; NUMBER OF SEQ ID NOS: 358				
; SOFTWARE: FastSEQ for Windows Version 4.0				
; SEQ ID NO 2				



; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-2

Query Match 89.9%; Score 545; DB 3; Length 113;
Best Local Similarity 92.9%; Pred. No. 2.9e-41;
Matches 105; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPKLLIYGVFIR 63
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QY 64 DSGVPDRFTGSGSGTDFTLTITSSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
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RESULT 3
US-10-144-644-45
; Sequence 45, Application US/10144644
; Publication No. US20030059429A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-10-144-644-45

Query Match 89.3%; Score 541; DB 4; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.6e-41;
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPKLLIYGVFIR 63
Db 1 ELVMTQSPSSLSVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGSGTDFTLTITSSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db 61 ESGVPDRFTGSGSGTDFTLTITSSVQAEDLAVYYCQNDHSYPFTFGSGTKLEIK 113

RESULT 4
US-10-700-740-45
; Sequence 45, Application US/10700740
; Publication No. US20040156850A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/700,740
; FILING DATE: 04-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-700-740-45

Query Match 89.3%; Score 541; DB 4; Length 113;  
Best Local Similarity 91.2%; Pred. No. 6.6e-41;  
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNRSNOKNYLAWYQQKPGQPPKLLIYGVFIR 63  
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Db 1 ELVMTQSPSSLVSAGEKVTMSCKSSQSLNRSNOKNYLAWYQQKPGQPPKLLIYGASTR 60

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Db 61 ESGVPDRFTGSGSGTDTLTITISSVQAE DLAVYYCQNDHSYPYTFGSGTKLEIK 113

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US-11-076-395-45  
; Sequence 45, Application US/11076395  
; Publication No. US20060029594A1  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; Appelbaum, Edward R.  
; Chaiken, Irwin M.  
; Cook, Richard M.  
; Gross, Mitchell S.  
; Holmes, Stephen D.  
; McMillan, Lynette J.  
; Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; Treatment of IL5 Mediated Disorders

; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp  
; STREET: P.O. Box 1539-UW2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/076,395  
; FILING DATE: 09-Mar-2005  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/10/700,740  
; FILING DATE: 04-Nov-2003  
; APPLICATION NUMBER: US/10/144,644  
; FILING DATE: 2002-08-08  
; APPLICATION NUMBER: US 08/470110  
; FILING DATE: 06-JUN-1995  
; APPLICATION NUMBER: US 08/467420  
; FILING DATE: 06-JUN-1995  
; APPLICATION NUMBER: US 08/363131  
; FILING DATE: 23-DEC-1994

; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50282-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5024  
; TELEFAX: 610-270-5090  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-11-076-395-45

Query Match 89.3%; Score 541; DB 6; Length 113;  
Best Local Similarity 91.2%; Pred. No. 6.6e-41;  
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNRSNOKNYLAWYQQKPGQPPKLLIYGVFIR 63  
:|||||  
Db 1 ELVMTQSPSSLVSAGEKVTMSCKSSQSLNRSNOKNYLAWYQQKPGQPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGSGTDTLTITISSVQAE DLAVYYCQNDHIYPYTFGGGTKLEIK 116  
:|||||  
Db 61 ESGVPDRFTGSGSGTDTLTITISSVQAE DLAVYYCQNDHSYPYTFGSGTKLEIK 113

RESULT 6  
US-10-340-189-2  
; Sequence 2, Application US/10340189  
; Publication No. US20030229207A1  
; GENERAL INFORMATION:  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Modified Antibody Variable Domains  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 W. Madison Street, 34th Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/340,189  
; FILING DATE: 10-Jan-2003  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/245,202A  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/082,842  
; FILING DATE: 23-JUN-1993  
; APPLICATION NUMBER: PCT/US92/10906  
; FILING DATE: 14-DEC-1992  
; APPLICATION NUMBER: US 07/808,464  
; FILING DATE: 13-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 88.4%; Score 536; DB 4; Length 113;  
Best Local Similarity 91.2%; Pred. No. 1.9e-40;  
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNRSNOKNYLAWYQQKPGQPPKLLIYGVFIR 63  
:|||||  
Db 1 DIVMTQSPSSLVSAGERVTMSCKSSQSLNRSNOKNFLAWYQQKPGQPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGSGTDTLTITISSVQAE DLAVYYCQNDHIYPYTFGGGTKLEIK 116  
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Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDHSHSYPLTFGAGTKLEIK 113

RESULT 7

US-10-325-696-2  
; Sequence 2, Application US/10325696  
; Publication No. US20040005630A1  
; GENERAL INFORMATION:  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Modified Antibody Variable Domains  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th Floor  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: United States of America  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/325,696  
; FILING DATE: 18-Dec-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/097,980  
; FILING DATE: 16-JUN-1998  
; APPLICATION NUMBER: 08/107,669  
; FILING DATE: 13-AUG-1993  
; APPLICATION NUMBER: PCT/US92/10906  
; FILING DATE: 14-DEC-1992  
; APPLICATION NUMBER: US 07/808,464  
; FILING DATE: 13-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janet M. McNicholas, Ph.D.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9050  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-325-696-2

Query Match 88.4%; Score 536; DB 4; Length 113;  
Best Local Similarity 91.2%; Pred. No. 1.9e-40;  
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGQPPKLLIYGVFIR 63

Db 1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLNSGNQKNFLAWYQOKPGQPPKLLIYGASTR 60

Qy 64 DSGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116

Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDHSHSYPLTFGAGTKLEIK 113

RESULT 8

US-11-133-775-2  
; Sequence 2, Application US/11133775  
; Publication No. US20050239141A1  
; GENERAL INFORMATION:  
; APPLICANT: Studnicka, Gary M.  
; TITLE OF INVENTION: Modified Antibody Variable Domains  
; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th Floor  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: United States of America  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/133,775  
; FILING DATE: 19-MAY-2005  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/097,980  
; FILING DATE: 16-JUN-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/107,669  
; FILING DATE: 13-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/10906  
; FILING DATE: 14-DEC-1992  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/808,464  
; FILING DATE: 13-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janet M. McNicholas, Ph.D.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9050  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 113 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-11-133-775-2

Query Match 88.4%; Score 536; DB 6; Length 113;  
Best Local Similarity 91.2%; Pred. No. 1.9e-40;  
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGQPPKLLIYGVFIR 63

Db 1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLNSGNQKNFLAWYQOKPGQPPKLLIYGASTR 60

Qy 64 DSGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116

Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDHSHSYPLTFGAGTKLEIK 113

RESULT 9

US-10-700-632-68  
; Sequence 68, Application US/10700632  
; Publication No. US20050118183A1  
; GENERAL INFORMATION:  
; APPLICANT: ImmunoGen, Inc.  
; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID  
; TITLE OF INVENTION: LEUKEMIA USING THE SAME  
; FILE REFERENCE: A8427  
; CURRENT APPLICATION NUMBER: US/10/700,632  
; CURRENT FILING DATE: 2003-11-05  
; PRIOR APPLICATION NUMBER: US 60/424,332  
; PRIOR FILING DATE: 2002-11-07  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 68

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; - LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-68
Query Match      88.4%; Score 536; DB 5; Length 115;
Best Local Similarity 91.2%; Pred. No. 1.9e-40;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNRSNQKNYLAWYQKPGQPPKLLIYGVFIR 63
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Db      1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLNLSGNQKNFLAWYQKPGQPPKLLIYGASTR 60
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QY      64 DSGVPDRFTGSGGTDFLTITSSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
      :|||||
Db      61 ESGVPDRFTGSGGTDFLTITSSVQAEDLAVYYCQNDHHSYPLTFGAGTKLEIK 113

RESULT 10
US-10-144-644-46
; Sequence 46, Application US/10144644
; Publication No. US20030059429A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION: INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
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US-10-144-644-46
Query Match      88.3%; Score 535; DB 4; Length 113;
Best Local Similarity 90.3%; Pred. No. 2.3e-40;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNRSNQKNYLAWYQKPGQPPKLLIYGVFIR 63
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Db      1 ELVMTQSPSSLSVSAGEKVTMSCKSSQSLNLSGNQKNYLAWYQKPGQPPKLLIYGASTR 60
      |||||

QY      64 DSGVPDRFTGSGGTDFLTITSSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
      :|||||
Db      61 ESGVPDRFTGSGGTDFLTITSSVQAEDLAVYYCQNDISYPTFTGSGTKLEIK 113

RESULT 11
US-10-700-740-46
; Sequence 46, Application US/10700740
; Publication No. US20040156850A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/700,740
; FILING DATE: 04-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-700-740-46
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Query Match      88.3%; Score 535; DB 4; Length 113;
Best Local Similarity 90.3%; Pred. No. 2.3e-40;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Qy	4	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSRNQKNYLAWYQQKPGQPPLLYGVFIR	63
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Db	1	ELVMTQSPSSLSVSAGEKVTMSCKSSQSLLNSGNQKNYLAWYQQKPGQPPLLYGASTR	60

Qy	64	DSGVPDRFTGSGSGTDFTLT	ISSVQAE	DLVY	QNDHI	YPYTF	GGTKLEIK	116
		:	:	:	:	:	:	
D6	61	ESGVPDRFTGSGSGTDFTLT	ISSVQAE	DLVY	QNDYS	YPYTF	GGTKLEIK	113

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RESULT 12
US-11-076-395-46
; Sequence 46, Application US/11076395
; Publication NO. US20060029594A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; Appelbaum, Edward R.
; Chaiken, Irwin M.
; Cook, Richard M.
; Gross, Mitchell S.
; Holmes, Stephen D.
; McMillan, Lynette J.
; Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; Treatment of IL5 Mediated Disorders
;

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US-11-076-395-46

Query Match 88.3%; Score 535; DB 6; Length 113;  
Best Local Similarity 90.3%; Pred. No. 2.3e-40;  
Matches 102; Conservative 5; Mismatches 6; Indels

Qy	4	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNLSNRNQNYLAWYQQKPGQPPKLLIYGVFIR	63
	:	:	:
D <sub>b</sub>	1	ELVMTQSPSSLSVSAGEKVTMSCKSSQSLNLSNRNQNYLAWYQQKPGQPPKLLIYGASTR	60

Qy	64	DSGVPDRFTGSGSGTDFTLTISSVQAE	DLAVVY	QNDHI	YPTFFGGG	KLEIK	116
		:	:	:	:	:	
Dp	61	ESGVPDRFTGSGSGTDFTLTISSVQAE	DLAVVY	QNDYS	YPFTFGSGG	KLEIK	113

RESULT 13  
US-10-144-644-16  
; Sequence 16, Application US/10144644  
; Publication No. US20030059429A1  
; GENERAL INFORMATION:  
; APPLICANT: Ames, Robert S.  
; APPLICANT: Appelbaum, Edward R.  
; APPLICANT: Chaiken, Irwin M.  
; APPLICANT: Cook, Richard M.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: McMillan, Lynette J.  
; APPLICANT: Theisen, Timothy W.  
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in  
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders

Query Match 86.8%; Score 526; DB 4; Length 113;

Best Local Similarity	89.4%;	Pred. NO. 1.5e-39;	Indels	0;
Matches	101;	Conservative	Mismatches	7;
			Gaps	0;

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Db	1	DI	V	M	T	Q	S	P	S	S	L	S	V	S	A	G	E	K	V	T	M	S	C	K	S	S	Q	S	L	N	S	G	N	K	N	L	A	W	Y	Q	K	P	G	Q	P	K	L	I	Y	G	A	S	T	60
QY	64	D	S	G	V	P	D	R	F	T	G	S	G	S	C	T	D	F	L	T	I	S	S	V	Q	A	E	D	L	A	V	Y	Y	Q	N	D	H	I	Y	P	T	F	G	G	T	K	L	E	I	K	116			
Db	61	E	S	G	V	P	D	R	F	T	G	S	G	S	C	T	D	F	L	I	S	S	V	Q	A	E	D	L	A	V	Y	Y	Q	N	V	H	S	F	P	F	T	F	G	S	G	T	E	L	E	I	K	113		

Search completed: May 19, 2006, 17:52:58  
Job time : 116.159 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 17:49:02 ; Search time 5.52381 Seconds  
(without alignments)  
44.858 Million cell updates/sec

Title: US-09-889-936A-8  
Perfect score: 606  
Sequence: 1 SRGDIVMTQSPSSLSVSAGE.....CQNDHIYPTFGGGTKLEIK 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
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8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	536	88.4	118	7 US-11-075-891-26	Sequence 26, Appl
2	516	85.1	113	7 US-11-219-563-71	Sequence 71, Appl
3	516	85.1	113	7 US-11-219-563-91	Sequence 91, Appl
4	483	79.7	113	7 US-11-219-563-72	Sequence 92, Appl
5	470	77.6	115	7 US-11-219-563-92	Sequence 2965, Ap
6	452.5	74.7	133	6 US-10-511-937-2965	Sequence 5, Appli
7	442	72.9	115	7 US-11-254-679-5	Sequence 23, Appl
8	412	68.0	107	7 US-11-221-902-23	Sequence 11, Appl
9	412	68.0	214	7 US-11-221-902-11	Sequence 63, Appl
10	404	66.7	101	7 US-11-221-902-63	Sequence 57, Appl
11	404	66.7	101	7 US-11-239-308-57	Sequence 17, Appl
12	391	64.5	107	7 US-11-221-902-17	Sequence 5, Appli
13	391	64.5	214	7 US-11-221-902-5	Sequence 7, Appli
14	391	64.5	214	7 US-11-221-902-7	Sequence 9, Appli
15	391	64.5	214	7 US-11-221-902-9	Sequence 6, Appli
16	391	64.5	254	7 US-11-075-891-6	Sequence 8, Appli
17	391	64.5	254	7 US-11-075-891-8	Sequence 10, Appl
18	391	64.5	254	7 US-11-075-891-10	Sequence 1, Appli
19	390	64.4	107	7 US-11-254-182-1	Sequence 28, Appl
20	386	63.7	110	7 US-11-075-891-28	Sequence 64, Appl
21	385	63.5	107	7 US-11-219-563-64	Sequence 5, Appli
22	383	63.2	107	7 US-11-254-182-5	Sequence 27, Appl
23	383	63.2	108	7 US-11-254-182-27	Sequence 23, Appl
24	383	63.2	108	7 US-11-219-121-23	Sequence 19, Appl
25	383	63.2	108	7 US-11-106-762-19	

26	383	63.2	214	7 US-11-219-121-27	Sequence 27, Appl
27	382.5	63.1	112	7 US-11-239-308-6	Sequence 6, Appli
28	382	63.0	107	7 US-11-219-563-66	Sequence 66, Appl
29	382	63.0	254	7 US-11-075-891-12	Sequence 12, Appl
30	382	63.0	254	7 US-11-075-891-14	Sequence 14, Appl
31	382	63.0	254	7 US-11-075-891-16	Sequence 16, Appl
32	381	62.9	107	7 US-11-219-563-67	Sequence 67, Appl
33	381	62.9	110	7 US-11-075-891-31	Sequence 31, Appl
34	380	62.7	107	7 US-11-219-563-63	Sequence 63, Appl
35	380	62.7	107	7 US-11-254-182-3	Sequence 3, Appli
36	380	62.7	113	7 US-11-239-308-4	Sequence 4, Appli
37	380	62.7	214	7 US-11-254-182-15	Sequence 15, Appl
38	380	62.7	217	7 US-11-254-182-23	Sequence 23, Appl
39	380	62.7	233	7 US-11-254-182-17	Sequence 17, Appl
40	379	62.5	107	7 US-11-219-563-50	Sequence 50, Appl
41	379	62.5	107	7 US-11-219-563-65	Sequence 65, Appl
42	379	62.5	107	7 US-11-219-563-68	Sequence 68, Appl
43	379	62.5	234	7 US-11-211-917-48	Sequence 48, Appl
44	378	62.4	171	6 US-10-981-300-10	Sequence 10, Appl
45	377	62.2	108	6 US-10-981-300-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-11-075-891-26  
; Sequence 26, Application US/11075891  
; Publication No. US20060088521A1  
; GENERAL INFORMATION:  
; APPLICANT: MAHADEVAN, DARUKA  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT  
; FILE REFERENCE: 263922US96  
; CURRENT APPLICATION NUMBER: US/11/075,891  
; CURRENT FILING DATE: 2005-03-10  
; PRIOR APPLICATION NUMBER: US 60/557,258  
; PRIOR FILING DATE: 2004-03-27  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 26  
; LENGTH: 118  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-11-075-891-26

Query Match	88.4%;	Score	536;	DB	7;	Length	118;
Best Local Similarity	91.2%;	Pred. No.	8e-25;				
Matches	103;	Conservative	3;	Mismatches	7;	Indels	0;
Gaps	0;						
Qy	4	DIWMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNVLA	WYQKPGQPPKLLIYG	VFIR	63		
Db	1	DIWMTQSPSSLSVSAGERVTMSCKSSQSLNSGNQKNFLAWY	QKPGQPPKLLIYG	ASTR	60		
Qy	64	DSGVPDRFTGSGSGTDTLTITSSVQAEDLAVYYCQNDHIY	PTFTGGG	TKLEIK	116		
Db	61	ESGVPDRFTGSGSGTDTLTITSSVQAEDLAVYYCQNDHSY	PLTFGAG	TKLEIK	113		

RESULT 2

US-11-219-563-71  
; Sequence 71, Application US/11219563  
; Publication No. US20060088539A1  
; GENERAL INFORMATION:  
; APPLICANT: Bander, Neil  
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC  
; FILE REFERENCE: 13651.001 (BZL-001)  
; CURRENT APPLICATION NUMBER: US/11/219,563  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: PCT/US04/06586  
; PRIOR FILING DATE: 2004-03-03



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; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-71

Query Match      85.1%; Score 516; DB 7; Length 113;
Best Local Similarity 88.5%; Pred. No. 9.8e-24;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY      4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
Db      1 DIVMTQSPSSLAVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQSPKLLIYWASTR 60

QY      64 DSGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db      61 ESGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDYSYPLTFGAGTKLELK 113

RESULT 3
US-11-219-563-91
; Sequence 91, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-91

Query Match      85.1%; Score 516; DB 7; Length 113;
Best Local Similarity 88.5%; Pred. No. 9.8e-24;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY      4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
Db      1 DIVMTQSPSSLAVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQSPKLLIYWASTR 60

QY      64 DSGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db      61 ESGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDYSYPLTFGAGTKLELK 113

RESULT 4
US-11-219-563-72
; Sequence 72, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
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; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
US-11-219-563-72

Query Match      79.7%; Score 483; DB 7; Length 113;
Best Local Similarity 81.4%; Pred. No. 6.5e-22;
Matches 92; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY      4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
Db      1 DIVMTQSPSSLAVSAGEKVTLSCKASESLNVGNQKTYVAWYQQKPGQSPKLLIYGASTR 60

QY      64 DSGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db      61 ESGVPDRFTGSGGTDFTLTISVQAEDLAVYYCGNSYSFPLTFGGGTKLELK 113

RESULT 5
US-11-219-563-92
; Sequence 92, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
US-11-219-563-92

Query Match      77.6%; Score 470; DB 7; Length 115;
Best Local Similarity 79.6%; Pred. No. 3.4e-21;
Matches 90; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY      4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQPPKLLIYGVFIR 63
Db      1 DIVMTQSQSSLAVSAGDKVTVCCKASQSLNVGSDKNYVAWYQAKPGQSPKLLIYSASTR 60

QY      64 DSGVPDRFTGSGGTDFTLTISVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db      61 ESGVPDRFTGSGGTDFTLTISVQAEDLAVYFCQNDNSYPLTFGAGTKLELK 113

RESULT 6
US-10-511-937-2965
; Sequence 2965, Application US/10511937
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OTHER INFORMATION: artificial sequence is derived from mouse and human antibody  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(107)  
OTHER INFORMATION: light chain variable region  
US-11-221-902-5

Query Match 64.5%; Score 391; DB 7; Length 214;  
Best Local Similarity 69.0%; Pred. No. 1.2e-16;  
Matches 78; Conservative 13; Mismatches 16; Indels 6; Gaps 1;  
QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLSNRNQKNYLAWYQKPGQPPKLLIYGVFIR 63  
Db 1 DIVMTQSPDSLAVSLGERATINCKASQSVSND-----VAVYQKPGQSPKLLISYTSR 54  
QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116  
Db 55 YAGVPDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQDYNPPTFGGGTKLEIK 107

RESULT 14  
US-11-221-902-7  
Sequence 7, Application US/11221902  
Publication No. US20060088522A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT  
FILE REFERENCE: 04000-0317285  
CURRENT APPLICATION NUMBER: US/11/221,902  
CURRENT FILING DATE: 2005-09-09  
NUMBER OF SEQ ID NOS: 89  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 7  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: artificial sequence is derived from mouse and human antibody  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(107)  
OTHER INFORMATION: light chain variable region  
US-11-221-902-7

Query Match 64.5%; Score 391; DB 7; Length 214;  
Best Local Similarity 69.0%; Pred. No. 1.2e-16;  
Matches 78; Conservative 13; Mismatches 16; Indels 6; Gaps 1;  
QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLSNRNQKNYLAWYQKPGQPPKLLIYGVFIR 63  
Db 1 DIVMTQSPDSLAVSLGERATINCKASQSVSND-----VAVYQKPGQSPKLLISYTSR 54  
QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116  
Db 55 YAGVPDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQDYNPPTFGGGTKLEIK 107

RESULT 15  
US-11-221-902-9  
Sequence 9, Application US/11221902  
Publication No. US20060088522A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT  
FILE REFERENCE: 04000-0317285  
CURRENT APPLICATION NUMBER: US/11/221,902  
CURRENT FILING DATE: 2005-09-09  
NUMBER OF SEQ ID NOS: 89  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 9  
LENGTH: 214

TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: artificial sequence is derived from mouse and human antibody  
OTHER INFORMATION: sequences  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(107)  
OTHER INFORMATION: light chain variable region  
US-11-221-902-9  
Query Match 64.5%; Score 391; DB 7; Length 214;  
Best Local Similarity 69.0%; Pred. No. 1.2e-16;  
Matches 78; Conservative 13; Mismatches 16; Indels 6; Gaps 1;  
QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLLSNRNQKNYLAWYQKPGQPPKLLIYGVFIR 63  
Db 1 DIVMTQSPDSLAVSLGERATINCKASQSVSND-----VAVYQKPGQSPKLLISYTSR 54  
QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116  
Db 55 YAGVPDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQDYNPPTFGGGTKLEIK 107  
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